

Copyright GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

Gencore version 5.1.6						
Copyright (c) 1993 - 2005 Compugen Ltd.						
MM protein - protein search, using sw model						
run on: February 14, 2005, 15:01:02 ; Search time 177 Seconds (without alignments) 1886.303 Million cell updates/sec						
result	No.	Score	Query	Match	Length	DB ID
1	3406	100.0	652	1	33CA_BACTK	
2	3212	94.3	659	1	C3BA_BACTO	
3	2341.5	68.7	644	1	C3AA_BACTT	
4	2341.5	68.7	652	2	Q9S6N9	
5	2337.5	68.6	652	2	Q6PXN8	
6	2319.5	68.1	652	2	Q643Z7	
7	2152	63.2	649	1	Q5744_BACTK	
8	1272.5	37.4	1144	2	QBKZL7	
9	1205.5	35.4	1157	1	CBAA_BACUK	
10	1166.5	34.2	1169	1	CBBA_BACUK	
11	1127.5	33.1	1157	1	C9CA_BACTO	
12	1124.5	33.1	1179	1	C1IB_BACTC	
13	1122	33.9	1229	1	C1BB_BACTU	
14	1122	32.9	1233	1	C1BC_BACTM	
15	1121	32.3	1215	1	C1KA_BACTM	
16	1119	32.9	1138	1	C7AA_BACTM	
17	1118.5	32.8	719	2	Q9F0FB	
18	1117	32.8	1138	1	C7AB_BACUK	
19	1115.5	32.8	1138	1	CLID_BACTU	
20	1112	32.6	1138	1	C7AB_BACUA	
21	1105	32.3	719	1	C1IA_BACTK	
22	1100.5	32.3	719	2	Q93N5	
23	1100.5	32.3	719	2	Q6X1B1	
24	1096.5	32.2	719	1	Q45708	
25	1094.5	32.1	719	2	Q8KY61	
26	1072.5	32.1	719	2	Q85796	
27	1071.5	31.5	1228	1	C1BA_BACTK	
28	1070.5	31.4	1228	2	Q93N5	
29	1060	31.1	1160	1	C8CA_BACTP	
30	1060	31.1	1160	2	Q6R2R6	
31	1053	30.9	1231	2	Q8KNY2	

run on: February 14, 2005, 15:01:02 ; Search time 177 Seconds
- protein search, using sw model
(without alignments)
1886.303 Million cell updates/sec

105	748.5	22.0	1118	2	Q9AMB81	09amb1 bacillus th	RL	App1. Environ. Microbiol. 58:3921-3927(1992).
106	745	21.9	1170	2	Q8QTC6	Q6q766 bacillus th	RN	[2] SEQUENCE FROM N.A.
	745	21.1	682	1	CJBA_BACTU	Q86170 bacillus th	RP	SEQUENCE FROM N.A.
107	700	20.6	381	2	Q45740	Q45740 bacillus th	RC	SEQUENCE FROM N.A.
108	685	20.1	1280	2	Q8VUK9	Q8vuk9 bacillus th	RA	STRAIN=NRRL B-18655 / EG5144;
109	679	19.9	1156	1	CJAA_BACTG	Q9901 bacillus th	RA	Donovan W.P., Rupar M.J., Slaney A.C.,
110	676.5	19.9	405	2	Q765X3	Q76533 paenibacill	RT	"Bacillus thuringiensis CRYIIC, (b) protein toxic to coleopteran
111	669.5	19.7	675	2	Q8KNV2	Q8kn2 bacillus th	RT	insects.",
112	669.5	19.5	675	1	CJAA_BACTI	P09652 bacillus th	RL	Patient number US5378625, 03-JAN-1995.
113	663.5	19.5	674	1	Q939T3	Q93933 bacillus th	CC	- - FUNCTION: Promotes collagendolytic lysis by binding to the midgut
114	663.5	18.4	1236	2	CJBA_BACTI	P05539 bacillus th	CC	epithelial cells of Coleoptera. Has moderate level of toxicity to
115	656.5	19.3	1136	1	CJBA_BACTI	Q6be03 bacillus th	CC	southern corn rootworm.
116	639	18.8	810	2	Q8VU03	P1640 bacillus th	CC	- - SUBUNIT: Monomer
117	639	18.7	1180	1	CJAA_BACTI	Q6bch5 bacillus th	CC	- - DEVELOPMENTAL STAGE: The crystal protein is produced during
118	631.5	18.5	675	2	Q8BCH5	Q9x682 bacillus th	CC	sporulation and is accumulated both as an inclusion and as part of
119	626.5	18.4	1109	1	CJAA_BACTF	Q87905 bacillus th	CC	the spore coat of the protein is located in the N-
120	625	18.4	674	1	CJAA_BACTU	Q8fd05 bacillus th	CC	- - MISCELLANEOUS: Toxic segment of the delta endotoxin family.
121	623.5	18.3	1128	2	Q8FDG0	Q8vul0 bacillus th	CC	- - SIMILARITY: Belongs to the delta endotoxin family.
122	613	18.0	1254	2	Q8VU0	Q8vw62 bacillus th	CC	- - SIMILARITY: Belongs to the delta endotoxin family.
123	604	17.7	666	2	Q8VW62	Q7x3f7 bacillus th	CC	- - This SWISS-PROT entry is copyright. It is produced through a collaboration
124	600.5	17.6	666	2	Q7X3F7	Q7x3f7 bacillus th	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
125	600	17.6	753	1	CJAA_BACUF	Q3221 bacillus th	CC	the European Bioinformatics Institute. There are no restrictions on its
126	594.5	17.5	683	2	Q75VA2	Q75va2 bacillus th	CC	use by non-profit institutions as long as its content is in no way
127	573.5	16.8	650	2	Q8VNX2	Q8vnx2 bacillus th	CC	modified and this statement is not removed. Usage by and for commercial
128	567.5	16.7	688	2	Q8VNX1	Q8vnx1 bacillus th	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
129	535	15.7	675	1	CJPA_BACTJ	Q87906 bacillus th	CC	or send an email to license@isb-sib.ch).
130	534	15.7	826	1	CJAA_BACUH	Q8s597 bacillus th	CC	- -
131	510	15.3	618	1	CJAA_CLOBI	Q05102 clostridium	CC	- - MISCELLANEOUS: Toxic segment of the delta endotoxin family.
132	483	14.2	1155	2	Q9AM80	Q9amb0 bacillus th	CC	- -
133	482	14.2	613	1	CGRA_CLOBI	Q45882 clostridium	CC	- -
134	472	13.9	1270	2	Q8VU1	Q8vul1 bacillus th	CC	- -
135	316	9.3	1257	1	CJCA_BACTU	Q45754 bacillus th	CC	- -
136	301	8.8	297	2	Q45789	Q45789 bacillus th	CC	- -
137	279.5	8.2	1245	1	CJPA_BACTU	Q45712 bacillus th	CC	- -
138	277.5	8.1	1286	2	Q8KZM2	Q8kzm2 bacillus th	CC	- -
139	272.5	8.0	1167	1	CJAA_BACTU	P56956 bacillus th	CC	- -
140	262	7.7	633	1	C2AD_BACTU	Q9rmq3 bacillus th	CC	- -
141	255.5	7.5	196	2	Q6SS54	Q6s554 bacillus th	CC	- -
142	251.5	7.4	633	2	Q6XF60	Q6kf60 bacillus th	CC	- -
143	248	7.3	633	2	Q956N5	Q9b6n5 bacillus th	CC	- -
144	247.5	7.3	193	2	Q6SS53	Q6s553 bacillus th	FT	3D-structure; Sporulation; toxin.
145	247.5	7.3	633	2	Q8GH90	Q8gh90 bacillus th	FT	Q > P (in strain EG5144).
146	245.5	7.2	633	1	C2DA_BACTK	P21253 bacillus th	FT	N > D (in strain EG5144).
147	245.5	7.2	633	2	Q71SV7	Q71sv7 bacillus th	FT	V > V (in strain EG5144).
148	245.5	7.2	633	2	Q8GHF3	Q8ghf3 bacillus th	FT	F > S (in strain EG5144).
149	245	7.2	633	1	C2AB_BACTK	P21254 bacillus th	FT	YV > IYF (in strain EG5144).
150	242	7.1	633	2	Q7X2S7	Q7x2s7 bacillus th	FT	S > G (in strain EG5144).
						Q7x2s7 bacillus th	FT	451. VARIANT S > G (in strain EG5144).
							FT	590. L > I (in strain EG5144).
							FT	600. K > I (in strain EG5144).
							FT	624. 624 K > T (in strain EG5144).
							FT	65. 79 HELIX 65 79
							FT	81. 81 HELIX 81 81
							FT	83. 86 HELIX 83 86
							FT	87. 88 HELIX 87 88
							FT	91. 98 HELIX 91 98
							FT	99. 99 HELIX 99 99
							FT	102. 103 TURN 102 103
							FT	105. 113 TURN 105 113
							FT	114. 114 TURN 114 114
							FT	115. 118 HELIX 115 118
							FT	119. 119 HELIX 119 119
							FT	124. 153 HELIX 124 153
							FT	156. 158 HELIX 156 158
							FT	161. 181 HELIX 161 181
							FT	182. 185 HELIX 182 185
							FT	188. 189 HELIX 188 189
							FT	191. 209 HELIX 191 209
							FT	210. 210 HELIX 210 210
							FT	211. 215 HELIX 211 215
							FT	223. 254 HELIX 223 254
							FT	255. 255 HELIX 255 255
							FT	260. 276 HELIX 260 276
							FT	277. 277 HELIX 277 277
							FT	281. 281 HELIX 281 281

ALIGNMENTS

RESULT 1
 C3BB_BACTU STANDARD; PRT; 652 AA.
 ID C3BB_BACTU
 AC Q06177; Q45717;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Pesticidal crystal protein cry3Bb (Insecticidal delta-endotoxin
 DE CRYIIB(b)) (Crystalline entomocidal protoxin) (74 kDa crystal
 DE protein). Name=cry3Bb; Synonyms=cryIIB(b), cryIIB2;
 OS Bacillus thuringiensis.

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

NCBI_TaxID=1428;

RN [1] SEQUENCE FROM N.A.

STRAIN=EG4961;

RC MEDLINE=93119147; PubMed=1476436;

RA Donovan W.P., Rupar M.J., Slaney A.C., Malvar T., Gawron-Burke M.C.,

RA Johnson T.B.,

RA "Characterization of two genes encoding Bacillus thuringiensis

insecticidal crystal proteins toxic to Coleoptera species.";

RT RT

FT	TURN	282	283	Qy	241	TDHCYNTWYNTGLNLGIRSTYDAWKNRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTEL	300		
FT	HELIX	284	287	Db	241	TDHCYNTWYNTGLNLGIRSTYDAWKNRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTEL	300		
FT	TURN	289	294	Qy	301	TRDIDPPIPLNTLQBYGPTFLS1BNSIRKPHLFPYLOG1EFHTLRLQPGYFGKDSFNYW	360		
FT	STRAND	296	297	Db	301	TRDIDPPIPLNTLQBYGPTFLS1BNSIRKPHLFPYLOG1EFHTLRLQPGYFGKDSFNYW	360		
FT	TURN	304	305	Qy	361	SGNYVETRSP1GSSKTTSPYGDKSTEYQKLSPQKVYRTIANTDVAWPNGKVYLG	420		
FT	HELIX	313	315	Db	361	SGNYVETRSP1GSSKTTSPYGDKSTEYQKLSPQKVYRTIANTDVAWPNGKVYLG	420		
FT	HELIX	316	318	Qy	421	VTKVDFSQYDDQKNETSTQYDSDKRNGHYSQDS1DQLPBPETDDEPLEKAYSHQNYAE	480		
FT	HELIX	322	326	Db	421	VTKVDFSQYDDQKNETSTQYDSDKRNGHYSQDS1DQLPBPETDDEPLEKAYSHQNYAE	480		
FT	TURN	327	328	Qy	481	CFLMDQRRGTP1PFETWTHRSVDFENTIDAKITOLPFPVKAVALSSGAS1BGPGFVGGNL	540		
FT	STRAND	336	348	Db	481	CFLMDQRRGTP1PFETWTHRSVDFENTIDAKITOLPFPVKAVALSSGAS1BGPGFVGGNL	540		
FT	TURN	351	352	Qy	541	LPLKESNS1AKFPTVTLNSALLQYRVRVYASTNRLFVQNSNDFLVYINTTMNK	600		
FT	STRAND	354	355	Db	541	LPLKESNS1AKFPTVTLNSALLQYRVRVYASTNRLFVQNSNDFLVYINTTMNK	600		
FT	STRAND	357	369	Qy	601	DDDLITYQTFDLATNSMGFSGDKNEBLIGAESFSYNEK1YD1K1EFPYQOL	652		
FT	TURN	371	372	Db	601	DDDLITYQTFDLATNSMGFSGDKNEBLIGAESFSYNEK1YD1K1EFPYQOL	652		
FT	STRAND	377	378	Qy	601	DDDLITYQTFDLATNSMGFSGDKNEBLIGAESFSYNEK1YD1K1EFPYQOL	652		
FT	STRAND	382	383	Db	601	DDDLITYQTFDLATNSMGFSGDKNEBLIGAESFSYNEK1YD1K1EFPYQOL	652		
FT	TURN	391	394	RESULT 2					
FT	TURN	396	397	C3BA_BACTO					
FT	STRAND	399	411	C3BA_BACTO					
FT	TURN	413	414	AC	P117569;	STANDARD;	PRT;	659 AA.	
FT	STRAND	417	430	AC	01-NOV-1990	(Rel. 16, Created)			
FT	TURN	431	434	AC	01-NOV-1990	(Rel. 16, Last sequence update)			
FT	STRAND	435	442	DT	05-JUL-2004	(Rel. 44, Last annotation update)			
FT	STRAND	450	454	DT	05-JUL-2004	(Rel. 44, Last annotation update)			
FT	HELIX	455	458	DE	Pesticidal crystal protein cry3Ba (Insecticidal delta-endotoxin				
FT	HELIX	468	471	DE	Cry1IB(a) (Crystalline entomocidal protoxin) (75 kDa crystal				
FT	STRAND	474	483	DE	Name=cry3Ba; Synonyms=cry1IB, cry1IB(a);				
FT	TURN	486	487	DE	Bacillus thuringiensis (subsp. tolworthi)				
FT	STRAND	490	498	OS	Bacilli; Firmicutes; Bactillales; Bacillaceae; Bacillus.				
FT	TURN	499	500	OC					
FT	TURN	503	504	OX					
FT	STRAND	506	506	RN	[1]				
FT	STRAND	512	516	RC	SEQUENCE FROM N.A.				
FT	HELIX	517	519	RC	STRAIN=3F;				
FT	TURN	522	523	RX	MEDLINE=90206811; PubMed=2320431;				
FT	STRAND	525	526	RA	SICK, A., Gaertner, F.H., Wong, A.;				
FT	STRAND	527	530	RT	"Nucleotide sequence of a coleopteran-active toxin gene from a new				
FT	STRAND	540	543	RL	isolate of Bacillus thuringiensis subsp. tolworthi."				
FT	STRAND	551	556	NR	Nucleic Acids Res. 18:1305-1305 (1990).				
FT	HELIX	559	562	CC	-1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut				
FT	STRAND	565	574	CC	epithelial cells of Coleoptera.				
FT	STRAND	578	584	CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during				
FT	TURN	585	586	CC	sporulation and is accumulated both as an inclusion and as part of				
FT	STRAND	589	594	CC	the spore coat.				
FT	TURN	600	601	CC	-1- MISCELLANEOUS: Toxic segment of the protein is located in the N-				
FT	HELIX	606	608	CC	terminus.				
FT	STRAND	610	613	CC	-1- SIMILARITY: Belongs to the delta endotoxin family.				
FT	STRAND	618	619	CC					
FT	STRAND	625	631	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
FT	TURN	636	637	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				
FT	STRAND	640	649	CC	the European Bioinformatics Institute. There are no restrictions on its				
SEQUENCE	652 AA;	74385 MW;	63048332CDE8CCC6 CRC64;	CC	use by non-profit institutions as long as its content is in no way				
SQ				CC	modified and this statement is not removed. Usage by and for commercial				
Query Match	100.0%	Score 3406;	DB 1;	CC	entities requires a license agreement (See http://www.18b-bib.ch/announce/				
Best Local Similarity	100.0%	Pred. No. 2..3e-214;	Length 652;	CC	or send an email to license@18b-bib.ch .				
Matches 652;	Conservative 0;	Mismatches 0;	Indels 0;	CC					
Db	1 MNPNRSEHDITKVTNSPLQTINHNOYPLADNPNSTLSEBLNYKEFLRNTDSSTEVDLNS	60		CC					
Qy	1 MNPNRSEHDITKVTNSPLQTINHNOYPLADNPNSTLSEBLNYKEFLRNTDSSTEVDLNS	60		CC					
Db	1 MNPNRSEHDITKVTNSPLQTINHNOYPLADNPNSTLSEBLNYKEFLRNTDSSTEVDLNS	60		CC					
Qy	61 TVDAVGTG1SYVGQIIGVGVPGAGLTSFYOSFLNTIWPSPADPKAFMAQVEVLDK	120		CC					
Db	61 TVDAVGTG1SYVGQIIGVGVPGAGLTSFYOSFLNTIWPSPADPKAFMAQVEVLDK	120		CC					
Qy	121 KIEEYAKSKA1AEQ1QONFEDYNNLWAKT1PL1SLRSKRSQDR1RELPSQAESHFRN	180		CC					
Db	121 KIEEYAKSKA1AEQ1QONFEDYNNLWAKT1PL1SLRSKRSQDR1RELPSQAESHFRN	180		CC					
Qy	181 SMPSAVSKPEVFLPTVQAANTHLL1KDAOVGEWGSSEDVAFYHROLKL1TQY	240		DR	X17123; CAA34983.1;				
Db	181 SMPSAVSKPEVFLPTVQAANTHLL1KDAOVGEWGSSEDVAFYHROLKL1TQY	240		DR	EMBL; A07234; CAA00645.1;				

DR	InterPro; IPR005638; endotoxin C.	OX	NCBI_TaxID=1444, 1441, 1435;
DR	InterPro; IPR005639; endotoxin N.	RN	[1] SEQUENCE FROM N.A.
DR	InterPro; IPR005639; Gal bind Like.	RP	SPECIES=B.t.tenebrionis;
DR	Pfam; PF001944; Endotoxin C; 1-	RC	MEDLINE=3658680;
DR	Pfam; PF00555; Endotoxin_M; 1.	RX	Hoefl H., Saurinck J., Houtven A. V., Vaect M.;
DR	Pfam; PF001945; Endotoxin_N; 1.	RA	"Nucleotide sequence of a gene encoding an insecticidal protein of
KW	Sporulation; Toxin; SEQUENCE; 659 AA; 75159 MW; 5A5B214FF84168CA CRC64;	RT	Bacillus thuringiensis var. tenebrionis toxic against Coleoptera.";
SQ	SEQUENCE; 659 AA; 75159 MW; 5A5B214FF84168CA CRC64;	RL	Nucleic Acids Res. 15:7183-7183(1987).
	Query Match Similarity 94.3%; Score 3212; DB 1; Length 659;	RN	[2]
	Best Local Similarity 93.7%; Pred. No. 1-2e-201; Matches 610; Conservative 22; Mismatches 19; Indels 0; Gaps 0;	RP	SEQUENCE FROM N.A.
Qy	1 MNPNNESEHDTIKVTPNSELQTNHNOYPLADNPNSTLEELNYKEPLRMTEDSSTEVLDNS 60	RC	SPECIES=B.t.tenebrionis;
Db	9 MNPNNESEHDTIKVTPNSELQTNHNOYPLADNPNSTLEELNYKEPLRMTADNSTEVLDSS 68	RA	Sekar V., Thompson D.V., Maroney M.J., Bookland R.G., Adang M.J.;
Qy	61 TVKDAYTGISVQGQILGVVGPFAGLTSFYQSFNLTINPSDADPWKAQAEVFLIDK 120	RT	"Molecular cloning and characterization of the insecticidal crystal protein gene of Bacillus thuringiensis var. tenebrionis.";
Db	69 TVKDAYTGISVQGQILGVVGPFAGLTSFYQSFNLAQPSDADPWKAQAEVFLIDK 128	RL	Proc. Natl. Acad. Sci. U.S.A. 84:7036-7040(1987).
Qy	121 KIEEYAKSKAALAOGLQNFEDYVNLNSWKTPLSLRSRQSDIREFSQAEQSHFRN 180	RP	[3]
Db	129 KIEEYAKSKAALAOGLQNFEDYVNLNSWKTPLSLRSRQSDIREFSQAEQSHFRN 188	RC	SEQUENCE FROM N.A.
Qy	181 SMPSFAVSKFEVLFPLTYAQAAANTHLLKDAQVGEKGYSSEDVAEFTYRQLKTOQY 240	RA	SPECIES=B.t.tenebrionis; STRAIN=NB176;
Db	189 SMPSFAVSKFEVLFPLTYAQAAANTHLLKDAQVGEKGYSSEDVAEFTYRQLKTOQY 248	RT	MEDLINE=95131759; PubMed=7830581;
Qy	241 TDHCVNWYNGNGLRGSTDAWKEVNFREREMTITVLDLIVLFPFYDIPLYSKGVKTEL 300	RA	Adams L.P., Mathews S., O'Hara P., Petersen A., Gurtler H.;
Db	249 TDHCVNWYNGNGLRGSTDAWKEVNFREREMTITVLDLIVLFPFYDIPLYSKGVKTEL 308	RT	"Elucidation of the mechanism of Cry11A overproduction in a mutantized strain of Bacillus thuringiensis var. tenebrionis.";
Qy	301 TRDIFDPFISLNTLQGYPLSIEINSIRPHFLDYLQGEFHTPLQGYFGDSFNTW 360	RA	RA
Db	309 TRDIFDPFISLNTLQGYPLSIEINSIRPHFLDYLQGEFHTPLQGYFGDSFNTW 368	RT	"Isolation and characterization of EG2158, a new nucleotide sequence of Bacillus thuringiensis toxic to coleopteran larvae, and the toxin gene.";
Qy	361 SGNYVTRPSTGSSKTITSPPYGDKESTEPPVQLSFDQKTYRTIANTDAWPGKTYLG 420	RT	RT
Db	369 SGNYVTRPSTGSSKTITSPPYGDKESTEPPVQLSFDQKTYRTIANTDAWPGKTYLG 428	Mol.	"Mutagenized strain of Bacillus thuringiensis var. tenebrionis.";
Qy	421 VTKVDFSOYDQNETSTQYDTSKRNGHVSQDSDQLPPTTDEPLEKASHOLNAYE 480	RT	RT
Db	429 VTKVDFSOYDQNETSTQYDTSKRNGYLGQDSDQLPPTTDEPLEKASHOLNAYE 488	Mol.	"Mutagenized strain of Bacillus thuringiensis var. tenebrionis.";
Qy	481 CPELMODRGTIPFPTWTHSVDFFNTDAEKITOLPVKAQASASIEBGPFTGGNL 540	RT	RT
Db	489 CPELMODRGTIPFPTWTHSVDFFNTDAEKITOLPVKAQASASIEBGPFTGGNL 548	Mol.	"Nucleotide sequence and deduced amino acid sequence of a coleopteran-active delta-endotoxin gene from Bacillus thuringiensis subsp. san diego.";
Qy	541 LPKKESSNSIAKEPVTLNSAALLQYRIVASTNLRLFQNSNDPLVYINKTMNK 600	RT	RT
Db	549 LPKKESSNSIAKEPVTLNSAALLQYRIVASTNLRLFQNSNDPLVYINKTMNK 608	Mol.	"Nucleotide sequence and deduced amino acid sequence of a coleopteran-active delta-endotoxin gene from Bacillus thuringiensis subsp. san diego.";
Qy	601 DDDLYTYQFDLATTNSNNGNGSGDNKELLIGAESFVSNEKTYIDKIEFIPVQ 651	RT	RT
Db	609 DDDLYTYQFDLATTNSNNGNGSGDNKELLIGAESFVSNEKTYIDKIEFIPVQ 659	Mol.	"Nucleotide sequence and deduced amino acid sequence of a coleopteran-active delta-endotoxin gene from Bacillus thuringiensis subsp. san diego.";
RESULT 3		RT	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
C3AA_BACTT		RP	SPECIES=B.t.tenebrionis;
ID_C3AA_BACTT		RC	MEDLINE=92049739; PubMed=1658659; DOI=10.1038/353815a0;
AC_P01130; P21255;		RA	Li J., Carroll J., Gilroy T.E., Sobieski D.A., Bennett B.D.,
DT 01-APR-1988 (Rel. 07, Created)		RT	"Nucleotide sequence and deduced amino acid sequence of a coleopteran-active delta-endotoxin gene from Bacillus thuringiensis subsp. san diego.";
DT 25-OCT-2004 (Rel. 45, Last sequence update)		RT	"Crystal structure of insecticidal delta-endotoxin from Bacillus thuringiensis at 2.5-A resolution.";
DE Pesticidal crystal protein cry3Aa precursor (Insecticidal delta-endotoxin Cry11A(a)) (Crystalline entomocidal protein) (73 kDa crystal protein).		RT	Nature 353:815-821(1991).
DE Name=cry3Aa; Synonyms=bt13, cry3A, cryC, cryIIIA(a);		RL	X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
OS Bacillus thuringiensis (subsp. tenebrionis),		CC	CC
OS Bacillus thuringiensis (subsp. morrisonii), and		CC	CC
OS Bacillus thuringiensis (subsp. san diego),		CC	CC
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		CC	CC

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use.

	FT	TURN	500	501
	FT	STRAND	503	504
	FT	STRAND	509	513
	FT	HELIX	514	516
	FT	STRAND	519	520
	FT	TURN	522	523
	FT	STRAND	525	527
	FT	STRAND	537	540
	FT	STRAND	544	550
	FT	STRAND	552	553
	FT	STRAND	560	569
	FT	STRAND	573	579
	FT	TURN	580	581
	FT	STRAND	582	589
	FT	TURN	595	596
	FT	HELIX	601	603
	FT	STRAND	605	608
	FT	STRAND	613	614
	FT	STRAND	619	625
	FT	TURN	629	630
	FT	STRAND	633	644
SQ	SEQUENCE	644 AA;	731	
Query Match				
Best Local Similarity				
Matches 446; Conservativ				
Qy	1	MNPNRSEHDITKV		
Db	1	MNPNRSEHDITKT		
Qy	61	TVKDAIGTGISVG		
Db	61	TTKQTKQGKISVG		
Qy	121	KIEEYAKSKAAL		
Db	120	KIADYAKNAKAAEL		
Qy	181	SMPSPAVSKFEVLF		
Db	180	SMPSFAISGYELP		
Qy	241	TDHCYMWYNGLNG		
Db	240	TDHCYKRWYNGLGDIC		
Qy	301	TRDITDPFISPL		
Db	300	TRDVLTDPIGVANN		
Qy	361	SGNYVETRPSIGSS		
Db	360	SGNYVSTRPSIGSN		
Qy	421	VTKVDEQSYDQKNN		
Db	419	VTKVDEQSYDQKND		
Qy	481	CFLMDRGRGTPFF		
Db	478	CFLMDGSRGTPVLL		
Qy	541	LEFLKESNSNIAKFK		
Db	538	IQCQE-NGSAATIYV		
Qy	601	DDDLTYQTDFLIAAT		
Db	596	GDTLTYNFSNLASPF		

Q9S6N9	PRELIMINARY;	PRT;	652 AA.	Db	546 IOCIE-NGSAATIYVT-PDVSYSQKYARIHYASTSSQTITFTLSLDGAPDNQYFDKTKINK 603
AC				Qy	601 DDDLTQYQFDLATTNSNGPQSGKRNELLIGAESFVNSKEKIVIDKIEFLPV 650
DT	01-MAY-2000 (T-EMBLrel. 13, Created)			Db	604 GDTLTYNSENLA5TSTPFLSG--NNLQGTVGLSAGDKVYDKEFIPV 651
DT	01-MAY-2000 (T-EMBLrel. 13, Last sequence update)				
DT	01-MAR-2004 (T-EMBLrel. 26, Last annotation update)				
DE	Cry3Aa protein.				
GN	Name=ry3Aa;				
OS	Bacillus thuringiensis.				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
OX					
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BT22;				
RA	Zhang J., Song F.P., Xie T.J., Wang X.M., Huang D.F.;				
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ231900; CAB41411.1; -.				
DR	PIR; A27323; A27323.				
DR	HSSP; P07130; IDLC.				
DR	GO; GO:0005102; F:receptor binding; IEA.				
DR	GO; GO:000512; P:defense response; IEA.				
DR	GO; GO:0009405; P:pathogenesis; IEA.				
DR	InterPro; IPR001178; Endotoxin.				
DR	InterPro; IPR005638; endotoxin_N.				
DR	InterPro; IPR008979; Gal_bind_Like.				
DR	InterPro; IPR00944; Endotoxin_C.				
DR	PFam; PF00345; Endotoxin_M; 1.				
DR	PFam; PF00345; Endotoxin_N; 1.				
DR	SEQUENCE 652 AA; 74035 MW;	544A161DDF7647 CRC64;			
Qy	Query Match 68.6%; Score 2341.5; DB 2; Length 652; Best Local Similarity 68.6%; Pred. No. 1.1e-144; Matches 446; Conservative 75; Mismatches 122; Indels 7; Gaps 6;				
Db	9 MNPNNRSEHDTIKVTPNSELQTNHMQYPLADPNNSTLEELVNYKEFLRMTDSSTEVLNDS 60				
Qy	1 MNPNNRSEHDTIKVTPNSELQTNHMQYPLADPNNSTLEELVNYKEFLRMTDSSTEVLNDS 68				
Db	61 TVKDAVGTRG1SUVQG1Q1LGVGVPPAGLTSFVQSFNTIWPSSADPMKAFNAQVEVLTID 120				
Qy	69 TTKDVIQKG1SUVG1LGVGFQGGALVSSFTNLFNTIWPSE-DPKMKFMEQVEALMDQ 127				
Db	90 KIEEYAKSKAKAELQGLQNLNFDDYVNA1NSWKTKPLSLRSRSQRDRRELFSQARESHFRN 180				
Qy	121 KIEEYAKSKAKAELQGLQNLNFDDYVNA1NSWKTKPLSLRSRSQRDRRELFSQARESHFRN 180				
Db	128 KADYAKRNKALABQGLQNLNFDDYVNA1NSWKTKPLSLRSRSQRDRRELFSQARESHFRN 187				
Qy	181 SMPSFAVSKFEVFLPFTYAQAANTHLLKDKAQVFGEEWGSSEDVAEFTHRQLKLQY 240				
Db	188 SMPSFAISQEVFLPFTYAQAANTHLLKDKAQVFGEEWGSSEDVAEFTHRQLKLQY 247				
Qy	241 TDKCWNWYNGLNGLRSGYTDANKENFRREMTLTVLDLIVLFPFTDRLYSKGKVTTEL 300				
Db	248 TDHKCVKWNVGLDKLRSGYTDANKENFRREMTLTVLDLIVLFPFTDRLYSKGKVTTEL 307				
Qy	301 TRD1FTDPFSNLTLQEVGPTFUSLNSIRKPHFLDYLQGIPBHTRLQGYFGKDSFNYW 360				
Db	308 TRDVLTDPPVGUNNLRGQYDGSKSTPVOCLSFDGKVTANTDVAAMPNGKTYLG 420				
Qy	361 SGNYVETRPSIGSSKTITSFYGDKSTPVOCLSFDGKVTANTDVAAMPNGKTYLG 420				
Db	368 SGNYVTRPSIGSSNDITSPYGNKSSSEPVQNLEFNGKEVYRAVANTMLAVPSA-VYSG 426				
Qy	421 VTKVDFSQDDQNETSTTYDSEKRNNCHVSA0DSIDOLPPTTDEPLKAYSHQNLNAYE 480				
Db	427 VTKVDFSQNDQTDSEKRNNCHVSA0DSIDOLPPTTDEPLKAYSHQNLNAYM 485				
Qy	481 CPMQDRRTIPFPTWHSVDNTTIDEAKITOLPVKAYALSSGASIEPGFTGKGNL 540				
Db	486 CPMQGSRRTIPVLTWTHKSVDFNMITSKKITQPLTKAYKLQSGASVAGRFTGDDI 545				
Qy	541 LFLKESNSPIAKFKVTLNSAALLQYRVRIRYASTNLRFLVQNSNDFLVYINKTMNK 600				
Db	542 VTKVDFSQNDQTDSEASTQYDSEKRNNCHVSA0DSIDOLPPTTDEPLKAYSHQNLNAYE 480				
Qy	547 VTKVDFSQNDQTDSEASTQYDSEKRNNCHVSA0DSIDOLPPTTDEPLKAYSHQNLNAYM 485				
Db	547 VTKVDFSQNDQTDSEASTQYDSEKRNNCHVSA0DSIDOLPPTTDEPLKAYSHQNLNAYM 485				

Qy	481	CFLMDRRTGRIPPFWTHRSYDFENTIDEAKITOLPVVKAIALSGASLIEGPOFTGGNL	540	Db	486	CFLMQGSRRTIPVPLTWTHKGSVDPNMDSKKIKTQLPLVKAYKLOSGASVVGPPFTGGDI	545		
Db	486	CFLMQGSRRTIPVPLTWTHKGSVDPNMDSKKIKTQLPLVKAYKLOSGASVVGPPFTGGDI	545	Qy	541	LELKESSNSIAKPKVTLNSAALLQYRVRIRYASTNTNLPLFQNSNNDELVIXINKTKMK	600		
Qy	541	LPLKESSNSIAKPKVTLNSAALLQYRVRIRYASTNTNLPLFQNSNNDELVIXINKTKMK	600	Db	546	IQCITE-NGSAATTIYT-PDVSYSQKRHRHYASTSQITFTLSIDGAPNNQQYEDKTINK	603		
Db	546	IQCITE-NGSAATTIYT-PDVSYSQKRHRHYASTSQITFTLSIDGAPNNQQYEDKTINK	603	Qy	601	DDDLTYQTPLATNSNMNGSGDKNELIGAEFSVSNKIVYDKEIFPV	650		
Qy	601	DDDLTYQTPLATNSNMNGSGDKNELIGAEFSVSNKIVYDKEIFPV	650	Db	604	GDTMTYNFPLASFSTPPELSG--NNLQIGVTSUAGDVKYIDKEIFPV	651		
Db	604	GDTMTYNFPLASFSTPPELSG--NNLQIGVTSUAGDVKYIDKEIFPV	651	RESULT 7					
				C3CA_BACTK					
				ID	C3CA_BACTK				
				AC	045744;				
				DT	30-MAY-2000 (Rel. 39, Created)				
				DT	30-MAY-2000 (Rel. 39, Last sequence update)				
				DT	05-JUL-2004 (Rel. 44, Last annotation update)				
				DB	Pesticidal crystal protein cry3C (Insecticidal delta-endotoxin in				
				DB	Cry3C(a) (Crystalline entomocidal protein) (73 kDa crystal				
				DE	protein).				
				GN	Name=cry3Ca; Synonyms=cry3C(a), cry3IId,				
				OS	Bacillus thuringiensis (subsp. kurstaki).				
				OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
				OX	NCBI_TaxID=29339;				
				RN	[1]				
				RP	SEQUENCE FROM N.A.				
				RC	STRAIN=BT1109P;				
				RA	MEBELINE-592164108; PubMed=1544571; DOI=10.1016/0378-1119(92)90457-2;				
				RT	Lambert B., Theunis W., Aghda R., Van Audenhove K., Decock C.,				
				RA	Jansens S., Seurinck J., Peferoen M.,				
				RT	"Nucleotide sequence of gene cry3IId encoding a novel coleopteran active crystal protein from strain BT1109P of Bacillus thuringiensis subsp. kurstaki".				
				RT	Gene 110:131-132 (1992).				
				RL	CC-1-FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of Coleoptera.				
				CC	CC-1-DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.				
				CC	CC-1-MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.				
				CC	CC-1-SIMILARITY: Belongs to the delta endotoxin family.				
				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
				CC	EMBL: X59797; CAR42469.1; -.				
				DR	P1R: JH0261; JH0261.				
				DR	HSSP: P07130; 1D1C.				
				DR	InterPro: IPR01178; Endotoxin.				
				DR	InterPro: IPR0056338; endotoxin C.				
				DR	InterPro: IPR0056339; endotoxin N.				
				DR	InterPro: IPR008779; Gal-bind_Tike.				
				DR	Pfam: PF03944; Endotoxin_C; 1.				
				DR	Pfam: PF00555; Endotoxin_M; 1.				
				DR	Pfam: PF03945; Endotoxin_N; 1.				
				KW	Sporulation; Toxin.				
				SQ	SEQUENCE 649 AA; 73026 MW; 8FF1FB47957AC49 CRC64;				
					Query Match Score 63.2%; DB 1, Length 649;				
					Best Local Similarity 62.2%; Pred. No. 2, 7e-12;				
					Matches 407; Conservative 95; Mismatches 142; Indels 10; Gaps 6;				
Qy	1	MNPNNRSEDTIKTPNSLQETQHNPQADNPNSTLPLVYKEFLMTEDSSTEVLIDNS	60	Db	1	MNPNNRSEDTIKTPNSLQETQHNPQADNPNSTLPLVYKEFLMTEDSSTEVLIDNS	60		
Qy	2	MNPNNRSEDTIKTPNSLQETQHNPQADNPNSTLPLVYKEFLMTEDSSTEVLIDNS	60	Db	1	MNPNNRSEDTIKTPNSLQETQHNPQADNPNSTLPLVYKEFLMTEDSSTEVLIDNS	60		

61	TYKDAVGTGIVSVQGILGVGVPEAGALTSTYOSFLNTIWISDADEPKWAKMAQEVLIDK 120	DR Pfam; PF03555; Endotoxin; N-1.
59	TPKDAIQKGISLIGDGVGVPEAGALTSTYOSFLNTIWISDADEPKWAKMAQEVLIDQ 117	DR Pfam; PF03945; Endotoxin; N-1.
	SEQUENCE 114 AA; 128660 MW; 98F93070C49014AB CRC64;	SO
121	KIBEYAKSRALABGLQIQLNFSWKKTPSILRSRSQDIRELQSQAESHFRN 180	Query Match Score 37.4%; Length 1144;
118	KIADYARDKATAEQLGKVNPFYDVSALDSNDKTPTLTRDRSGNIRELPSQAESHFR 177	Best Local Similarity 40.9%; Pred. No. 2.1e-74;
		Matches 284; Mismatches 222; Indels 73; Gaps 19;
181	SMPSFAVSKFEVLFLPFTAQAANTHLLKDAQVFLGEWYSSDEDVAFYFLRQLKTOQX 240	Query 1 MNPNNRSEHDITIKTPNSLQTNINQXPLADNPNSTLLESLNQKEFLRMTEDSSTEVLDNS 60
178	SMPSFAVSGEVFLPFTAQAANTHLLKDAQVFLGEWYSSDEDVAFYFLRQLKTOQX 237	1 MSPNNQNEYLLDASSSTSDNSYRPLANTDQTTLQMNQYDYLMSGENPFLFGNP 60
241	TDHCVCVNTVNGVNGLRSYTDAYWKFLKFRRENTLTVLDLTLFLPFDIYSLGKVKTEL 300	Qy 61 TV---KDAVGTGIVSVQGILGVGVPEAGALTSTYOSFLNTIWISDADEPKWAKMAQEV 116
238	TNFKAKVYKRAGLQKLRGTYEEVVKFNRYRRENTLTVLDLTLFLPFLDVTYTKGVKTEL 297	Db 61 ETPISSSTVQGIGIVGVQYLGALGVPEAGQIASFSYFIVQLWPSTSTVSYEMIMKQVED 120
301	TRDIFTDPFSLNLTQLEYQPTFUSIENSIRKPHFLFDYQFLQGKQDSFNYW 360	Qy 117 LIDKKEEYAKSKALABLGQIQLNFSWKKTPSILRSRSQDIREL---FS 172
298	TRDVLTDPTPVAVNNMNGGTTFSNTENYIRKPHFLDYLHQFLHSRLQPGFQGTDSEFNYW 357	Db 121 LIDQK1TDSVTKTALLGLQJGDLQFLVQYSLSKWL---NNDPEARSVYVYQI 173
361	SGNYVETRSIGSSRTTISPFYQDKSTPVPQKLPSFGOKVYRTIANTDVAAMPNG---K 416	Qy 173 QAESHRNNSMPSFAVSKFEVLFLPFTAQAANTHLLKDAQVFLGEWYSSDEDVAFYHHR 232
358	SGNYVSTRSIGSSDDEIRSPFVGNKSTLDVQNLLENGEKVFRAVANGNLAVMPVGTCGTK 417	Db 174 ALELDVAKTSPFASQBYVPLLSVAQAANLHLILRLDASIFGAEWGFPGEISTFYDR 233
417	YLGCTTIVKPSQYDQKNETSTOTYDSKRNGHVAQDPSIDQPPERTDEPLKAIKSHQI 476	Qy 233 QKLTQOXTDQCVNNVNGLNGLRSSTYDAWKENKFRREMTLTVDLTLVLPFPFLDYL 292
418	IHSGTVKIQFSQNDRKDVTRTQYDTSKRNVGGI -VPSIDQLPPTTDESLEKAIKSHQI 476	Db 234 QVTRTAQYSDICVKNVNTGLDKLKGTTNAASWLYKHFRRRENTLTVLDLVALFPNTDRTY 293
477	NYAECFLMQRGRTIPTFFFWTHRSVDFPFTTDAEKITOPVTKAYALSGASLIEGPGFT 536	Qy 293 SKGVKVELTRDIFTDQI-----FSLNLTOQEYQPTFUSIENSIRKPHFLDYL 338
477	NYVRCFLLGGRGIIIPVFWTHRSVDFPFTKAYALSGASLIEGPGFT 536	Db 294 PIETTQLTREVYDPIVNRBTSGFCRRLNSLNS---DISFSEVAVSRSPHFSFIDL 349
537	GGNLFLKKESSNSTAKFKTLLNSALLQPRYRIRYASTNLRLFVQNSNNDFLYIINK 596	Qy 339 QGIEFH---TRLOQGYFGKDSFMYWGNVYTRPSIGSSK----TTS---PFY---GDKS 386
537	GGDLIKTCNTG -GLTLYVTPAPDLYTSSKTYKIRYASQVRFIDSYTHSISFED 595	Db 350 SRIEFYTTAGLPLNNTTELEYWVGHSIKYKNTNASSALERNYGTTSNKKYDILANKD 409
597	TMDKGNTLTYNSENLISSVSRPIEISGG-NKIGVSQGGGDEVYIDKIEFIPM 648	Qy 387 TEPVOKLSEFDGOKVYRTIANTDVAAMPNGKTYLGTGTVKDFQYDQKNETSTQ---TYDTSK 444
596	TMDKGNTLTYNSENLISSVSRPIEISGG-NKIGVSQGGGDEVYIDKIEFIPM 648	Db 410 1 FQVRSIJDALANYY-----AQYI-GVYDASFTILDKNTGSGSVGGFTYSKP 455
		Qy 445 RNNHGHSAQ---DSIDQLPPTTDEPLKAYSHOLNAYAECFLMQD----RGTIPPTF 496
		Db 456 HTMVOCTQNTNTDIPPE---NEPSURGYSHRLSHTSYSESKNASSPARYGNLPPFAW 513
		Db 632 AFTPEANTSDSLTVGADSASGGAVYDKEFLIPV 665
	RESULT 8	
Q8KZL7	PRELIMINARY; PRT; 1144 AA.	
Q8KZL7	01-OCT-2002 (TREMBurel. 22, Created)	Qy 497 TRSVDIFPENTDAEKITOPVTKAYALSGASLIEGPGFTGGNLFLKESSNSTAKFKY 556
Q8KZL7	01-OCT-2002 (TREMBurel. 22, Last sequence update)	Db 514 TRSADAVTNTVYSDKLTQIOPVYKTAHLVSGTIVKRGFTGNCNL-KRTSSCPLATSVS 572
Q8KZL7	01-NAR-2004 (TREMBurel. 26, Last annotation update)	Qy 557 IMAAIIQYRVRIRYASTNQRLFVQNSNNDFLYIINKDDLTYQFDLATTNS 616
		Db 573 VRS -PLSORYRARIYASTNQRLFVQNSNNDFLYIINKDDLTYQFDLATTNS 616
		Qy 617 NMGFSGDKNELLIGAESFSNEKIVYDKEFIPV 650
		Db 632 AFTPEANTSDSLTVGADSASGGAVYDKEFLIPV
	RESULT 9	
CBAK_BACUK	STANDARD; PRT; 1157 AA.	
ID_CBAK_BACUK	AC Q45704;	
	DT 16-OCT-2001 (Rel. 40, Created)	
	DT 16-OCT-2001 (Rel. 40, Last sequence update)	
	DT 05-JUL-2004 (Rel. 44, Last innovation update)	
	DE Pesticidial crystal protein cryBAA (Insecticidal delta-endotoxin	
	DE CryVIIA(a) (Crystalline entomocidal protein) (131 kDa crystal	
	DE protein)	
	GN Name=cry8Aa; Synonyms=cryVIIA(a);	
	OS <i>Bacillus thuringiensis</i> (subsp. <i>kumamotoensis</i>)	
	OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
	NCB _TaxID=132267;	
	[1]	
	RN SEQUENCE FROM N.A.	
	RP STRAIN=SPS-502;	
	RC "A strain of <i>Bacillus thuringiensis</i> subsp. <i>galleriae</i> (Coleoptera: Scarabaeidae)."	
	RA "A strain of <i>Bacillus thuringiensis</i> subsp. <i>galleriae</i> (Coleoptera: Scarabaeidae)."	
	RT novel cry8 gene highly toxic to <i>Anomala cuprea</i> (Coleoptera: Scarabaeidae)."	
	RT "A strain of <i>Bacillus thuringiensis</i> subsp. <i>galleriae</i> (Coleoptera: Scarabaeidae)."	
	RT novel cry8 gene highly toxic to <i>Anomala cuprea</i> (Coleoptera: Scarabaeidae)."	
	Biol. Control 28:191-196 (2003).	
	EMBL: AB089299; BAC07226.1; .	
	HSSP: Q06117; 1J16.	
	GO: GO:0005102; P: receptor binding; IEA.	
	GO: GO:0006952; P: defense response; IEA.	
	GO: GO:0009405; P: pathogenesis; IEA.	
	InterPro: IPR009079; 4 helix cytokine.	
	InterPro: IPR001178; Endotoxin.	
	InterPro: IPR005638; endotoxin C.	
	InterPro: IPR005639; endotoxin N.	
	InterPro: IPR00879; Gal_bind_Like.	
	Pfam: PF03944; Endotoxin C; 1.	
	PFAM: PF03944; Endotoxin C; 1.	

RA	Payne J.M., Sick A.J., Foncerra da L.;	Qy	512 ITQLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1	570
RT	"Novel coleopteran-active <i>Bacillus thuringiensis</i> isolate and a novel gene encoding a coleopteran-active toxin.";	Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1	582
RL	Patent number EP0498537, 12-AUG-1992.	Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE	626
CC	-1- FUNCTION: Promotes coleopteran-dosmotic lysis by binding to the midgut epithelial cells of Coleoptera.	Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637	
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650	
CC	-1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	Db	638 IILSMGDFSSQEVYIDRIEFIPV 661	
CC	-1- SIMILARITY: Belongs to the delta endotoxin family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	U04364; AAA21117.1; -.			
DR	HSSP; P07130; 1D1C.			
DR	InterPro; IPR001178; Endotoxin.			
DR	InterPro; IPR005638; endotoxin_C.			
DR	InterPro; IPR005639; endotoxin_N.			
DR	InterPro; IPR008919; Gal_bind_Like.			
CC	PF03944; Endotoxin_C; 1.			
DR	PFam; PF00555; Endotoxin_M; 1.			
DR	PFam; PF03945; Endotoxin_N; 1.			
KW	SPORULATION; Toxin.			
SEQUENCE	1157 AA; 131009 MW; 687B05C49DBE93683B CRC64;			
Qy	35.4%; Score 1205.5; DB 1; Length 1157;			
Best Local Similarity	39.2%; Pred. No. 5.3e-70; Gaps 21;			
Matches	268; Conservative 135; Mismatches 224; Indels 57; Gaps 21;			
Db	1 MNPNNRSEHDITKWPNSLQTNHNOYPLADNPNSTLEENLYKEFLRMTEDSSTEVLDNS 60			
Qy	1 MSPNNQNEYEIIDATPSPVSQDSNRPANEPPTDALQNNYKDYLKNSGGENDELFGNP 60			
Qy	61 TV--KDAVGTVGSVVGQTGILGVYGPAGALTSPYQSFLNTIWS-DADPKWAKMAQEV 116			
Db	61 EPTISSSTTGTGIGVGRILALGVPUFQASQYSPFVQLWFSKSDIVGEIMERVE 120			
Qy	117 LIDRKIEYYAKSALAAELQGLQNNFEDYNAWSKCKPLSLRSKSDPDRRELFSOAS 176			
Db	121 LVIQKIEKTVKDIALKGQNALDVIQSLDWE--NRNDRARTSVSNQFIALD 177			
Qy	177 HFRNSMPSFAVKSPKEVLF1PTYAQAAQANTHLLKDAQVFGEEGNSSEDAEYFHRQLKU 236			
Db	178 NFVSSIPSFAVSGHEVLLVAVQAQVNLHLLRDASTFGEENGFTPGIISRFYNRQVQ 237			
Qy	237 TQOYTDHCWVNWVNGLNGLGRSTYDAWVKNFREREMTLTVLDLIVLPFEDYRYSKV 296			
Db	238 TAEYSDYCVKWYKIGLDKUKTFSKSWLNHQFRERMLLVLVLDLVALFNYDTHMPIET 297			
Qy	297 KPEBLTRDIFTDPI-FSLNLTQY-----GPTFLSIS-IRKPHLFDYLOGIEFHTR 346			
Db	298 TAATLTDYTDPAFNIVTSGCNPWSTHSGLLFYEVENVTRPHLFDILSSEVINTS 357			
Qy	347 LQPGYFGKDFSF-NWMSGNYVETRPSIGSKKTTISPFYGDKSTPQVQLSF----DGQKV 400			
Db	358 RGGITLNDAYINWWSGHTLYKERTADSTVTTYAN-YGRITSE---KNSFALEDRDIPI 413			
Qy	401 YRTIANTDVAWPNKGKTYLGTVKDFQSDQKNETSTOT---YDSKRN--NGHVSADS 455			
Db	414 NSTVANL-----ANYQKAYGPGSNFHMVKRGTSSTTAYLSKTHTALQGCTQVYES 466			
Qy	456 IDOLPPETTDEPLEKAYSHQLYNAECAFLMQDR---RGTIPFFTWTHRSVDFENTIDAEK 511			
Db	467 SDDIPDRT-VPAEISHLRSHATSHSFNSKNSAYGCGSPVWTHTSADLANTIYSPK 525			
Qy	513 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Qy	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy	627 LIGAESEPSVSNEKYYIDKIEFIPV 650			
Db	638 IILSMGDFSSQEVYIDRIEFIPV 661			
Qy	512 ITOLPVVKAYALSSGAST1IEGPFTGGNNLFLKESNSI-AKFKVTLNSAALLQPYRVR1 570			
Db	526 ITQIPAVKQGDMILYLGGSVYQGPFTGGDI-LLKRTPSLGTFAVTVN-GSLSQSYRVR1 582			
Qy	571 RYASTNIR- LEVQNS -NNPDLVIVNKTMRKDDDTYQTFLATINSNMGSGDRNE			
Db	583 RYASTDFFEFTYLGDITKEKRF---NKTMDNGASLTYETFKFASFIFTDFQFRETQDK 637			
Qy				

Db	61	EVPLSEQDAVKAADIVGKLTGGLPFVGVSPVSVLYTQLTDLWPKQKQSWEITMEQVE	120	CC - the Colorado potato beetle.
Qy	116	VLIDKKELEYAKSKALABLOGIQLQNNFDYVNALNSPDKTPLSLRSRSQRDIRELFSQA	175	CC - DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
Db	121	ELINQKIAEYARNKAISLELEGUNQYQLYTALEEKENPQNSGRALRD--VRNRFIELD	177	CC - MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus
Qy	176	SHFRNSMPSFAYSKEVFLPLTYAQANTHILLLKDAQVFGSEWGSSEDAEFTYHROK	235	CC -1- SIMILARITY: Belongs to the delta endotoxin family.
Db	178	SUFTQMPSPRFTINFEYFPFLTYTMANLHLLRASISFEGWGRSTSTINNNYNNRQMC	237	CC - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to licensee@isb-sib.ch).
Qy	236	LTOQYDHCVWVNVGLNGLGSSTYDAWKENFPEREMTILYLDLIVLFPFYDIRLYSKG	295	CC -
Db	238	LTAEYSDHCVWVYETGLAKLKGKSSAKWIDYNQFPEREMTILYLDVVALEFSNYDTRTYP	297	CC -
Qy	296	VKTELTDIIFTDP-----IFSINTLQYGPPTLSEI-SIRKPHFLDYLGBFHTPLQ	349	CC -
Db	298	TAQLIREVYDTPLGAVDPNIGSWTDKAPSSEIEKAARPHFVDYIQLTVTAKRS	357	CC -
Qy	350	GYFGKDSF-NYMSGNYVETRSPSIGSSKTTSFPGDKSTPEVQKLSFDDGKQVYRTIANT	408	CC -
Db	358	--FTSDYMRWYAGHQISYK-HIGTSSTFTOMYGTQNQLQSTSNEFTNDIYKTLNSGA	414	CC -
Qy	409	V--AAMPNGKTY- LGVTKYDFQSYDDQKNETSTQTYDSKRNNNGHVSQADSIDQLPPT	463	CC -
Db	415	VLLDIVYP-GTYYTFFSMPETEFMNLQNLNTRKLTYKAPSKDILDRTRSEELLPPT	473	CC -
Qy	464	TDEPLEKAYSHQLNAYECFLMDDRGTIPTFTWTHSVDFFNTDAKIKTOLPVKAYA	523	CC -
Db	474	SGQPNYESYSHRLIGHTFIVSSSTSSTVPSWTHRSADLTNTVKSGETIQPGGKSSTI	533	CC -
Qy	524	SSGASITLGPGFTGGNLLFLKESNSNSTAKVYKTVLNSAALORYVRIRYAS--TINLRLF	581	CC -
Db	534	GRNTYIIGKRGTYGDLVATDRIGS-CFQNIIPPS--ORFRIRYANETSYISLY	589	Qy 1 MNPNNEHEDTIKVTPNTSELQTNHN-QYPLADNPNTSLELNKVEFLRMTEDSSIEVLDN 59
Qy	582	VQNSNN--DFLVYINKTMMKDDLYQTFD-----LATTNNSNMGFSGDRNELLIGAE	633	Db 1 MNRNNQNEYELID-AFHCGCPSDDVTYRPLASDPNQALQNNYKQDYLQMTDEDYTSYIN 59
Db	590	GLNQSGTLKFKNQTYNSNKEN--DLTNYDFKTYEPRVISYNA---SSNQRLSSTGQ-	641	Qy 60 STV---KDAVGTGASVVGQILGVVPGFAGLTSEYQSFLNTVW-SDAPPWKAQMV 114
Qy	634	FVSNEKTYI--DKTEFIPY	650	Db 60 PSLISGRDAVQATLTIVGRILGALGVPFSGQIVSFEYQFLINTLWVNDNTAWEFMRQV 119
Db	642	--TNTNLNFIIDRTEFIPY	657	Qy 115 EVLIDKIEEYAKSKALAELOGLQNNEFEDVNAWSKTPLSLRS - KRSQSDRIRELFSQ 173
Db			Db 120 EELVNGQITEFARNQNLARLQGLDSFNTYQVSLQWV---LADRNDTNLSUVRAQFIA 175	
Qy			Qy 174 AESHPNSMPSFAVSKFEVFLPLTYAQANTHLLKDAQVFGEGKYSSEDVAEYHRO 233	
Db			Db 176 LDLDFTNAIPLFAVNQQQVPLPSVYQAVNHLHLKLDASLGEGWGFQOEISTYDRQ 235	
Qy			Qy 234 LKLTOQYTDHCUNWNTVNGLNGLGSSTYDANVKENFPEREMTILYLDLIVLFPYDYLRYL 293	
Db			Db 236 LELTAKTNYCETWNTGLDRLRGTMTESNLYRHQFREMTLWVLDVVALFPYDYLRYP 295	
Qy			Qy 294 KGVKTCBLTRDIFTDPF----SLNLTYQEVCP----TFLSLENS - TRKPHLFDFYLOGIEF 343	
Db			Db 296 TGSNPQLTREVYDTPVFNPPANVGLCRRNGTNPTNTSELENAFRTRPHFLDRNLSLTI 355	
RESUL11			Qy 344 HTRLQCPGFKDSENYWSGNYVETRSPSIGSSKTISPFY-----GDKSTPEVQ 391	
C9CA_BACTO		STANDARD;	Db 356 SSNRFP--VSSNEMDWSGTLR--RSYLSLDAVQDSYGLITTRATINGVGDGTRNIE 411	
ID	C9CA_BACTO		Qy 392 KLSFDQKQVTRTIANTDVAMPNGKTYLGLGTKVDFQYDOKNESTQTYDSKRNNGHVS 451	
AC	Q45733;		Db 412 STAVDRSALIGYGYNRASTVPGGFLFNGT-----SPANGGCRD 451	
DT	30-MAY-2000 (Rel. 39, Created)		DT 452 AQDSIDOLPPETTDEPLEKAYSHQLNAYECPLMQDR-----GTLIPFTWTHRSVDF 504	
DT	05-JUL-2004 (Rel. 44, Last annotation update)		RL 452 LYDNTNDELPPDES--TGSSTHRLSHVTPFSQTQAGSTANAGSVPTVWTRRDYDNL 507	
DE	Pesticidal crystal protein cry9Ca (Insecticidal delta-endotoxin CryIXCa) (Crystalline entomocidal protein) (130 kDa crystal protein)		-1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of Lepidoptera larvae. Has a fairly broad spectrum of activity against members of the Pyralidae, Sphingidae and Noctuidae families. It was the first insecticidal crystal protein characterized with activity against cutworms. No activity is observed against some beetles, such as	
DE	Name=cry9Ca, Synonyms=cry7XC(a),		CC 505 NTIDAKKTOITOLPVYKAYALSGASIE-----TAKFKVTLNSALLQ 564	
GN	OS Bacteria: Firmicutes; Bacilli: Bacillales; Bacillaceae; Bacillus		Db 508 NTITPNRITQPLVKAASAPVSGTIVLKGPFGGGIL-RRTTNGTFTLRTVTVNS-PLTQ 565	
OX	NCBI_TaxID=1442;			
RN	[1]			
RP	SEQUENCE FROM N.A. , AND PARTIAL SEQUENCE.			
RC	SEQUENCE FROM N.A. , AND PARTIAL SEQUENCE.			
STRAIN	BTSD0618A;			
RX	Medline=96141404; PubMed=8572715;			
RX	Lambert B., Buyse L., Decock C., Jansens S., Piens C., Saeij B., Peferoen M. ; Seurinck J., Van Audenhove K., "A Bacillus thuringiensis insecticidal crystal protein with a high activity against members of the family Noctuidae." ; Appl. Environ. Microbiol. 62:80-86(1996).			
CC	-1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of Lepidoptera larvae. Has a fairly broad spectrum of activity against members of the Pyralidae, Sphingidae and Noctuidae families. It was the first insecticidal crystal protein characterized with activity against cutworms. No activity is observed against some beetles, such as			

Qy	565	RYVRVIRYASTTNLRLPVQNSNNDELVYINKTNKDDDLTYQTF--DLATT--NSNM	618	51 ---IDPFVASTIQTGIGAKLGLTGYPPAGQIASLYSFILEBLWPKGSKQWBFIFMEH 107
Db	566	QYRLQYRPFASTGKQFIRVLRGGSIGVQFRRGTSKNGQELTYEEFTRFTTIGPENPPF	625	114 VEVLIDKKEEYAKSALKALELOGIQQNNFEDVYALNSKKTPTLSRSKRSQDRIELFLSQ 173
Qy	619	GFSGDKNEELIIGAEEFVSNKPIYIDKIEFPV	650	108 VEEETINQKILTYAARNKALSDLRGIGDALAVHESLWVE--NRNNTARSVYKQYTA 164
Db	626	TFTQARQEILTVNAECSVSTGSEYYIDRIEVFPV	657	174 AESHFRNMSMPSPAVSKFSTFLPTYAQANTHILLKDRQVFGREMGYSSSEDAEAFYHQ 233
RESULT 12				
C11B_BACTB	ID	C11B_BACTB	STANDARD;	PRT; 719 AA.
AC	Q45709;	DT	30-MAY-2000 (Rel. 39, Created)	Db 293 LKJUQOYTDHCIVAWYNGLRS-TYDAWKFNFRFRENTLTVLDTLVFPFDYRILS
DT	30-MAY-2000 (Rel. 39, Last sequence update)	Db 225 VERTDYSDHICIKWYNTGUNLRGTAWSWRINQFRKDMTLWVLDLVAFPSYDTLVYP		
DT	05-JUL-2004 (Rel. 44, Last annotation update)	Qy 294 KGVTTELTDIIFTDPIFSNLNTQEX-----GPTFLSIENS-TRKPHLFDFYLGQIEF		
DE	Pesticidal crystal protein cry1b (Insecticidal delta-endotoxin	Db 285 IKTSQLTREVYDIAIGVHPNQAFASTTWYNNNAPSAEAVIRSPHLLDPLEKVTI		
DE	Cry1(b) (Crystalline entomocidal protoxin) (81 kDa crystal protein)	Qy 344 HTRLQPGYFGKDSFNNYWSGNVYETRPSIGSSKTTISPFYGDKST--EPVQKLSFGQKRYV		
GN	Name=cry1b; Synonyms=cry1I(b), cryV, cryV465;	Db 345 YSLIS--RVSNTQYMMWGHRLUSRPICGALANTSQ--GSTMNTSINPV-TLQTSRVDY		
OS	Bacillus thuringiensis (Subsp. entomocidus)	Db 402 RTIANTDAAWPNGKVLGQVTKDPSQYDDQKNETSTOYDSRKNNGHVA--QDSLD 457		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	Db 400 RTESLAGINLNLPTQPNV-GVPRVDP--HWEKPTPLIASDNFVYLYGAGVGTQLDSEN		
OX	NCBI_TaxID=1436;	Qy 458 QLPPTTDEPLEKAYSHOLNAYACFCFLMQDRRGTFPFTWTHRSYDFFNTDAEKITOLPV		
RN	SEQUENCE FROM N.A.	Db 455 ELPPETTGOPNYSYSHRUSHIGLISASHVKALV--YSWTHRSADRTTIEPNSITQIPL		
RC	STRAIN=BP465;	Qy 518 VKGAYALSSGASLIEFPGFGTGNNLFLKEKSSNSTAKFOTLNSAALQYRVRKAYASTIN		
RX	MEDLINE=95314293; PubMed=7793960;	Db 513 VKAQFNLSGCAAVYRGPFQGDYL-RRNTGTFQGDYL-RRNTGTFQGDYL		
RA	Shin B.-S., Park S.-H., Choi S.-K., Koo B.-T., Lee S.-T., Kim J.-I.;	Qy 578 LRLFVQ----NSNDPLVYINKTMKDDDLTYQTDLATNSNMGFSGDNKNEILIGA		
RT	"Distribution of cryV-type insecticidal protein genes in <i>Bacillus</i> thuringiensis and cloning of cryV-type genes from <i>Bacillus</i> subsp. thuringiensis subsp. kurstaki and <i>Bacillus</i> thuringiensis subsp.	Db 571 LQHTTSINGKAINQGN----FSATMNNGEDLDYKTFRTIGFTPPFSFSDVQSTFTGA		
RT	entomocidus";	Qy 632 ESEVSNEKUYIDKIEFIPVQL		
RT	Appl. Environ. Microbiol. 61:2402-2407 (1995).	Db 625 WNFGSGNEVYDRIEFVFPVVE		
CC	-I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of certain coleopteran and lepidopteran species.	RESULT 13		
CC	Active on <i>Pluteella xylosteella</i> but not on <i>Bombyx mori</i> .	C11B_BACTU STANDARD; PRT; 1229 AA.		
CC	-I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	AC Q15739;		
CC	-I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	DT 30-MAY-2000 (Rel. 39, Created)		
CC	-I- SIMILARITY: Belongs to the delta endotoxin family.	DT 30-MAY-2000 (Rel. 39, Last sequence update)		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC	EMBL: U07642; AAA2114.1; -.			
DR	HSSP; P02965; 1C1V.	DB 513.1 Cry1B(b) (Crystalline entomocidal protoxin) (140 kDa crystal protein).		
DR	InterPro; IPR001118; Endotoxin.	DB Name=cry1Bb; Synonyms=cryET5, cry1B(b);		
DR	InterPro; IPR005638; endotoxin_C.	OS Bacillus thuringiensis is.		
DR	InterPro; IPR005619; endotoxin_N.	OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
DR	InterPro; IPR008919; Gal_bird_Like.	OX NCBI_TaxID=1428;		
DR	Pfam; PF03944; Endotoxin_C; 1.	RN SEQUENCE FROM N.A.		
DR	Pfam; PF00555; Endotoxin_M; 1.	RP STRAIN-NRL B-2110 / EG5847;		
DR	Pfam; PF03945; Endotoxin_N; 1.	RC Donovan W.P., Tan Y., Jany C.S., Gonzalez J.M. Jr.;		
KW	Sporulation; Toxin.	CC "Bacillus thuringiensis cryet4 and cryet5 toxin genes and proteins toxic to lepidopteran insects";		
SQ	SEQUENCE 719 AA; 81295 MW;	CC Patent number US322687, 21-JUN-1994.		
Qy	1 MNPNTRNREHTDTI-----KVTPNSELQTMHNQYPLADNPNSTEELNYKEFARMEDDS	CC -I- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae.		
Db	1 MKLKNPDKHQSLSSNAVKYIATDS-----LKNTDIELKNNNNEDYLRMSESES 50	CC -I- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.		
Qy	54 TEVDLNSTVKDAVGTGIVSIVGQ1Q1GVVSVFAGALTSPYQSINTNTWPSADDEWKAHQ 113	CC -I- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			

between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC DR EMBL; L32020; AAA22344.1; - .

CC DR HSSP; P02965; IC1Y.

CC DR InterPro; IPR001178; Endotoxin.

CC DR InterPro; IPR005638; endotoxin_C.

CC DR InterPro; IPR005639; endotoxin_N.

CC DR InterPro; IPR008979; Gal_bind_Like.

CC DR InterPro; IPR03944; Endotoxin_C; 1.

CC DR PFam; PF003555; Endotoxin_M; 1.

CC DR PFam; PF003945; Endotoxin_N; 1.

CC KW Sporulation; Toxin.

CC SQ SEQUENCE 1229 AA; 139769 MW; A4C949DB675C3269 CRC64;

Query Match Score 32.9%; Best Local Similarity 36.7%; Pred. No. 1.7e-4; Matches 247; Conservative 126; Mismatches 248; Indels 52; Gaps 16;

Query 1 MNPNNRSSHSDT1KTPNSELQINHNOVPLADNPNSTLEELAKYKEFIRTEEDS---STEV 56

Db 1 MTSNRKNEII-----NALSIPTVSNPST---QMNLSPDARI-ENSLCYAEVNN 46

Query 57 LDNSTVKDAVGTCISVYQOLQGVGVYPFAGALTFSYOSFLNTIWPSPDADPMKAQVEV 116

Db 47 IDPFVSASTVQFQINAGRILGVGPQGLASFTYSPFLGELWPGRDPMEIFLEHVEQ 106

Query 117 LDDKKBAYAKSKAELQGLQNNEFEDYVNALNSWKTPSLRSKRSQDRTRLEFSQAES 176

Db 107 LTRQVQTNTTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 177 HFNSMSPFAVSKPEVLEPLPTYAQANTHLLKKDAQVGEWCGYSSEDVAEPYHQLK 236

Db 164 DTTAIPFLRIRNEEVPLMYAQAAANHLLLRDASLFGWMASSDNQYYQOIRY 223

Query 237 TQOYTDHCVNWNVGLNLRGSTDYAWKVNFRERFLTVLTLVFPFDIIRLYSKGV 296

Db 224 TEYVSNHCVQWNTGLNLRGTAESWLNRYNQFRDLTGVLDLFPSTDTRTPINT 283

Query 297 KTELTTRDIFTDPI-----FSLNTLQEXGFPTFLSIENS-TKPHFLDYLQGIEBTHR 346

Db 284 SAQITREIYDPLGRTNAPSGFASTWNENNAPSFSA1EAAFRPHPLDPEQLTYS- 342

Query 347 LQPGYFGKDSENTWGNVYETRPSIGSKITSPFYGDKSTPVOQLSFGDKVYRTIAN 406

Db 343 ASSRWSSTOHMNTWGHRLNFRPQIGGTNTLSTOGTLNTNTSINPV-TLQFTSDRVIRENS 401

Query 407 TDVAAPNGKVKVQGTVKD-----FSQYDDQK-NESTOTYDTSKRNNNGHSAQDSIDOL 459

Db 402 A-----GTMNLLFTTPVNGVPWARFNTPNQVYNTGRTTSPQYQGVGQIQLFDSETEL 454

Query 460 PPETTDEPFLKAYSHOLNAYAECFLMQDRGTIBFFTWHTRSVDFNTIDAEKITOLPVVK 519

Db 455 PPETTDEPFLKAYSHOLNAYAECFLMQDRGTIBFFTWHTRSVDFNTIDAEKITOLPVVK 519

Query 520 AYALSSGAS1IEGPFGTGGNLLFLKEKSSNSIAKPKVTLNSAAILQYRVRVIRYASTINLRL 579

Db 513 ALNLHSGTvvGGFTGDDIL-RRTNTCTFGDIRLNNN-VPLSQRTRVIRYASTIDLQ 570

Query 580 LFVQNSNNDFLVIYINKTMKDDDLTYQFDLATTNSNMNGFSQDKNEELIGAESFVNEK 639

Db 571 FETTINGTGNIGNSRNTNGDNLEYRSTAGFSTPENFLNAQSTFTLGAQSF-SNOE 629

Query 640 IYIKIEFPVQL 652

Db 630 VYIDRVEFVPAEV 642

CC DR RN RP SEQUENCE FROM N.A. Bishop, A.H.; Bone, B.J.; Ellar, D.J.; RA RT "Cloning of novel *Bacillus thuringiensis* delta-endotoxin." ; DR RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases. -!- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects.

CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.

CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.

CC -!- SIMILARITY: Belongs to the delta endotoxin family.

CC -----

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC -----

DR EMBL; 246442; CAA86568_1; - .

DR HSSP; P02965; IC1Y.

DR InterPro; IPR001178; Endotoxin.

DR InterPro; IPR005638; endotoxin_N.

DR InterPro; IPR005639; endotoxin_N.

DR InterPro; IPR008979; Gal_bind_Like.

DR Pfam; PF03944; Endotoxin_C; 1.

DR Pfam; PF00555; Endotoxin_M; 1.

DR Pfam; PF03945; Endotoxin_N; 1.

DR Sporulation; Toxin.

CC SEQUENCE 1233 AA; 14051 MW; 7318382413529F21 CRC64;

Query Match Score 32.9%; Best Local Similarity 36.7%; Pred. No. 1.7e-4; Matches 247; Conservative 126; Mismatches 248; Indels 52; Gaps 16;

Query 1 MNPNNSEHDNTIKVTNSELQTNHQYPLADNPNSTLEELNYKEFIRMTDS---STEV 56

Db 1 MTSNRKNEII-----NALSIPTVSNPST---QMNLSPDARI-ENSLCYAEVNN 46

Query 57 LDNSTVTKDAVGTCISVYQOLQGVGVYPFAGALTFSYOSFLNTIWPSPDADPMKAQVEV 116

Db 57 LDNSTVTKDAVGTCISVYQOLQGVGVYPFAGALTFSYOSFLNTIWPSPDADPMKAQVEV 116

Db 107 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 117 LIDKKBAYAKSKAELQGLQNNEFEDYVNALNSWKTPSLRSKRSQDRTRLEFSQAES 176

Db 117 LIDKKBAYAKSKAELQGLQNNEFEDYVNALNSWKTPSLRSKRSQDRTRLEFSQAES 176

Db 107 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 123 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 123 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 131 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 131 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 139 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 139 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 147 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 147 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 155 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 155 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 163 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 163 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 171 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 171 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 179 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 179 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 187 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 187 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 195 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 195 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 203 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 203 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 211 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 211 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 219 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 219 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 227 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 227 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 235 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 235 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 243 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 243 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 251 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 251 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 259 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 259 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 267 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 267 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 275 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 275 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Query 283 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Db 283 LTRQVQTNTTAAIRLGLGRGLGRGYRQYQQAEL-----NENDAARSITLERYVALE 163

Qy	347 LQPGYFGKDSFNYWSGNVYETRPSIGSSKRITTSPTYGDKSTPVGQKLSSDGQKVYRTIAN	406	DR Pfam; PF03945; Endotoxin_N; 1.
Db	343 ASSRSSTSQQMNYWGHRLNFRPGGTNTTISQGLTNNTSINPV-TLQTSRDRYRTSEN	401	KW Sporulation; Toxin.
Qy	407 TDVAAPNGKRYLGTVKND-----FSQYDDQK-NETSTOTYDYSKRNNGHVSQAQSDTQD	459	SEQUENCE 1215 AA; 137378 MW; 7CAF7A3311893D9B CRC64;
Db	402 A-----GTMNLLPTPVNGVUPWARPNFNPQNVIYERGATTYSOQYGVGQLQFDSETL	454	Query Match 32.9%; Score 1121; DB 1; Length 1215;
Db	405 PPETTDEPPEKAYSHOLNTAECFLMDRGTIPPTWTRSVDFNTIDAEKCTQPLVK	519	Best Local Similarity 37.9%; Pred. No. 1. 9e-64;
Qy	520 AYALSSGASLIEGPPTFTGNNFLPKESSNSIAKEPKVTLNSAALLQYRVRIRASTNLR	579	Matches 251; Conservative 126; Missmatches 247; Indels 38; Gaps 16;
Qy	513 ALNLHSGVTVGGPQFTGGDIL-RRTNTGFDGDLRNLIN-VPLSQRQYRVRIRASTDQ	570	Qy 1 MNPNRSHDHTKIVTPNSELQTNHNOYPLADNPNSTLEBLNYKEFLRMTEDSSTEVLDDNS 60
Db	455 PPETTDEPPEKAYSHOLNTAECFLMDRGTIPPTWTRSVDFNTIDAEKCTQPLVK	512	Db 1 MNSRKRNEBIIANLISIPAVSNISQMDL--SPDARIE----DSLCVAEGNN--IDPF 50
Qy	580 LFVQNSNNDFLVITYINKTMNKDDDLTYQTQFDLATTNSNNNGFSGDQKNEILIGAESFVSNEK	639	61 TVKDAVETGTSIVVQGQILGVGVPGFAGALTSPYQSFQSLNTIWPSADPKAQMVAEVLID 119
Qy	571 FFTRINGTTNIGNFSRTRNQRGDNLEYRSPRTAGFSTPPNLFNAQSTFTLGAOSF-SNQ	629	Qy 51 VSASTVQGISTAGRILGTVLGVPGFAGQLAQSFYQSFQSLNTIWPSADPKAQMVAEVLID 119
Qy	640 IYDQKIEFPVQL 652		Db 51 KKEEBYAKSKALLELQGLQNNFEDYVNALNWSWCKTPLSRKSQDRRELFSQAEHSFR 179
Db	630 VYDREVEFVBAEV 642		Db 111 QQTDSVYRDTAIARLEGQGRGYSYQQALETWD--NRNDARSRSIRERYTALELDIT 167
			180 NSMFSFAVSKFEVLFPTVQAQANTHLLLKDQVFGEWGYSSEDAVEFYHROLKLTCQ 239
Qy			Qy 180 NSMFSFAVSKFEVLFPTVQAQANTHLLLKDQVFGEWGYSSEDAVEFYHROLKLTCQ 239
Db			Db 168 TAFLFSIRNEEYPLMVAQAAANLHLILRDLASLFGSEWMGMSADVQYQDQIYTEE 227
			Qy 240 YTDHCWVNNVNGLNGLRGSTYDAWKENFRERMTLTLDLIVLPFPEYDILYSKGVKTE 299
			Db 228 YSNHCWQYNTGQNLRLGTTAETWVYQNRDQLDVALVPSDTRTPPTAQ 287
			Qy 300 LTRDIFTDPIFSL---NTLQBYQGPFLSIENS-IRKPHFLDVLQGLEFHTRLQPGYFGK 354
			Db 288 LTREVYTDPGNQVAGPNNSWFRNGASFAEIAENAIQRPHLYDLTNTLYTR--RSQVGT 345
			Qy 355 DSNWWSGRVYETRPSIGSSKTTSPYFGDKSTEP--YOKLSPDGQKTYRTIANTDVAAW 412
			Db 346 TIANLWAGRHTPNRIOQGS---TSEMVYGAATNPNVSYDIPPNVDYRTVSLAGGJGS 402
			Qy 413 PNGKVLGVTKYDFSQYDQKNETSTQYDSKRNNGH---VSAQDSIDOLPPTTDBPL 468
			Db 403 LSGIRY-GIUTRVDMDIFMRNHPD1V7GIF--YHPGHAGIATQYKSDTELPPTTEQFN 458
			Qy 469 EKAYSHQNLNYAECPLMQRDRGTIPFTWTHRSYDFNTIDAEKITQPVVKAYLSSGAS 528
			Db 459 YRAFSLHISH--MGPITQDVPVSYWTHOSADRTNTINSDRTOPLVKHTLQSCTT 516
			Qy 529 IIRGPQFTGGDIL-RRTSGGPFAFSVNLN-FLKESSSNIAKEPKVTLNSAALLQYRVRIRAYSTNLRLFVQNSNND 588
			Db 517 VPKGPQFTGGDIL-RRTSGGPFAFSVNLN-FLKESSSNIAKEPKVTLNSAALLQYRVRIRAYSTNLRLFVQNSNND 588
			Qy 589 FLYIYINKTMNKDDDLTYQTQFDLATTNSNMGFGSDQKNEILIGAESFVSNEKLYIDKIEFI 618
			Db 575 IFAQGFDKTMMDAGAPLITQFSYSTATNAAFTPBRSSSLTIGDFTSGNEYVYDREFL 634
			Qy 649 PV 650
			Db 635 QV 636
			RESULT 16
			CTAA_BACTU STANDARD; PRT; 1138 AA.
			ID CTAA_BACTU Q03749; 30-MAY-2000 (Rel. 39, Created)
			DT 30-MAY-2000 (Rel. 39, Last sequence update)
			DE pesticidal crystal protein gene cryka (Insecticidal delta-endotoxin CryIK(a)) (Crystalline entomocidal protoxin) (137 kDa crystal protein). Name=cryka; Synonyms=cryk, cryk(a, b, c); OS Bacillus thuringiensis (subsp. morrisoni). Bacteria; Firmicutes; Bactillales; Bacillaceae; Bacillus. OC
			OX NCBI_TaxID=1441; NCBI_TaxID=1441;
			RP SEQUENCE FROM N.A.
			RC STRAIN=F190;
			RX MEDLINE=96102856; PubMed=8586263; DOI=10.1016/0378-1097(95)00397-1;
			RA Koo B.T., Park S.H., Choi S.-K., Shin B.S., Kim J.I., Yu J.H.;
			RT "Cloning of a novel crystal protein gene cryk from Bacillus thuringiensis subsp. morrisoni." PEMS Microbiol. Lett. 134:159-164 (1995).
			CC -1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of insects. Selectively toxic to <i>Artogeia rapae</i> but not active in <i>Plutella xylostella</i> .
			CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
			CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
			CC -1- SIMILARITY: Belongs to the delta endotoxin family.
			CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.iss-sib.ch/announce/ or send an email to license@iss-sib.ch).
			CC RESULT 16
			CC CTAA_BACTU STANDARD; PRT; 1138 AA.
			ID CTAA_BACTU Q03749; 30-MAY-2000 (Rel. 39, Created)
			DT 30-MAY-2000 (Rel. 39, Last sequence update)
			DE pesticidal crystal protein cry7Aa (Insecticidal delta-endotoxin CryVIIA(a)) (Crystalline entomocidal protoxin) (129 kDa crystal protein).
			GN Name=cry7Aa; Synonyms=cryIIIC, cryVIIA(a, b);
			OS <i>Bacillus thuringiensis</i> .
			OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
			OX NCBI_TaxID=1428;
			RN [1]
			RP SEQUENCE FROM N.A.

RX	MEDLINE=92384571; PubMed=1514800;	Soetaert P.; Peferoen M.;
RA	Lambert B.; Rofté H.; Panny K.; Jansens S.;	"Novel Bacillus thuringiensis insecticidal crystal protein with a silent activity against coleopteran larvae."
RT	Appl. Environ. Microbiol. 58:2536-2542 (1992).	
RL	-1- FUNCTION: Promotes colloidolytic lysis by binding to the midgut epithelial cells of Coleoptera. This protein is not toxic in its natural form. It is highly toxic to Colorado potato beetle larvae after an in vitro solubilization and trypsin activation step.	
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	
CC	-1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	
CC	-1- SIMILARITY: Belongs to the delta endotoxin family.	
CC	-1- -	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation, the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).	
CC	-1- -	
CC	DR M64478; AAA22251_1; -;	
CC	DR M67236; CAA0646_1; -;	
CC	DR P07130; A48944; A48944.	
CC	DR HSP5; P07130; IDLC.	
CC	DR InterPro; IPR001178; Endotoxin.	
CC	DR InterPro; IPR005638; endotoxin_C.	
CC	DR InterPro; IPR005639; endotoxin_N.	
CC	DR InterPro; IPR008979; Gal bind_like.	
CC	DR PF03294; Endotoxin_C_1.	
CC	DR PF00555; Endotoxin_M_1.	
CC	DR PF03045; Endotoxin_N_1.	
CC	KW Sporulation; Toxin.	
CC	SEQUENCE 1138 AA; 129391 MW;	69D8676D476A1FAC C9664;
Qy	Query Match 32.9%; Score 1119; DB 1; Length 1138;	
Db	Best Local Similarity 36.8%; Pred. No. 2.4e-64;	
Db	Matches 251; Conservative 120; Mismatches 237; Indels 74; Gaps 19	
Qy	1 MNQNRSEHDITKVTPNSELQTNHQQYPLADNPNSTLEELNYKRFURMTEDSSTEVILDNS 60	
Db	1 MNQNRSEHDITKVTPNSELQTNHQQYPLADNPNSTLEELNYKRFURMTEDSSTEVILDNS 60	
Qy	61 TWRDAVGTGIVGQILGVGVGPFGALTSVYQSFINTIWPMSDAPMKAQVEVILDK 120	
Db	61 TWRDAVGTGIVGQILGVGVGPFGALTSVYQSFINTIWPMSDAPMKAQVEVILDK 120	
Qy	56 NT--AINTVYVSTGATLSALGSPITNQYKLAGLWPWPGTIDWEMTEVILIDQ 113	
Db	56 NT--AINTVYVSTGATLSALGSPITNQYKLAGLWPWPGTIDWEMTEVILIDQ 113	
Qy	121 KIEEYAKSKAELZQGLONNFDDYVNLNSW--KRTPLLSRSRSQDIRELNSQASH 177	
Db	121 KIEEYAKSKAELZQGLONNFDDYVNLNSW--KRTPLLSRSRSQDIRELNSQASH 177	
Qy	114 KIEEYVRKKAIAELDQGSAALDKYQKLADWLGQDPEALSLVATEFRI----TDSL 167	
Db	114 KIEEYVRKKAIAELDQGSAALDKYQKLADWLGQDPEALSLVATEFRI----TDSL 167	
Qy	178 FRNSMSPFAVSKPEVFLIPTYQAOAANTHLLJKDAOVFGEWGKISSVEDAFTYRQLKT 237	
Db	178 FRNSMSPFAVSKPEVFLIPTYQAOAANTHLLJKDAOVFGEWGKISSVEDAFTYRQLKT 237	
Qy	168 FEFIMPSPKVTGEPBLPTVYQAOAANHLLAIRDSTLYGDKWGFNONIEENTYRQKRI 227	
Db	168 FEFIMPSPKVTGEPBLPTVYQAOAANHLLAIRDSTLYGDKWGFNONIEENTYRQKRI 227	
Qy	238 QQTSDHCYUNWYNGVGLNGHRSAYDANTKENFRFRENTLTVDLTVLFPIRILYSGVYK 291	
Db	238 QQTSDHCYUNWYNGVGLNGHRSAYDANTKENFRFRENTLTVDLTVLFPIRILYSGVYK 291	
Qy	228 SESDHCKWYNGVGLNGHRSAYDANTKENFRFRENTLTVDLTVLFPIRILYSGVYK 287	
Db	228 SESDHCKWYNGVGLNGHRSAYDANTKENFRFRENTLTVDLTVLFPIRILYSGVYK 287	
Qy	> 298 TEPLRDIDTPPSLNTQIQLQYGETFLSLEN-SIRKPHFLDYLOGIEFH-----R1Q 348	
Db	> 298 TEPLRDIDTPPSLNTQIQLQYGETFLSLEN-SIRKPHFLDYLOGIEFH-----R1Q 348	
Qy	288 TQLTREVYTDPSLISNPDGGSFSQMENTAIRTPHLVDLYIYTTSKYKAFSHEIQ 347	
Db	288 TQLTREVYTDPSLISNPDGGSFSQMENTAIRTPHLVDLYIYTTSKYKAFSHEIQ 347	
Qy	349 PGYFGKDSFNYWGSNNYVETRPSIGSSKITSPPYGDKSTEPVQK- LSFQDGQKQYRTIAN 406	
Db	349 PGYFGKDSFNYWGSNNYVETRPSIGSSKITSPPYGDKSTEPVQK- LSFQDGQKQYRTIAN 406	
Qy	348 PDLF-----YWAHAKVSPKKS-EQSNLTYTGTG-YK-TSGVTSIGSFGCNDYRTLIA 398	
Db	348 PDLF-----YWAHAKVSPKKS-EQSNLTYTGTG-YK-TSGVTSIGSFGCNDYRTLIA 398	
Qy	407 TDVAWAPNGKVKLYGTVYKVDPSQYDDQNETSTDSKRNNHHSQASDQLPPTIDE 466	
Db	407 TDVAWAPNGKVKLYGTVYKVDPSQYDDQNETSTDSKRNNHHSQASDQLPPTIDE 466	
Qy	400 PSSVYVTPQNY-GVEQVBFYGVKGHIVYRGDKYD-----LTYDSDQLPPD--GE 445	
Db	400 PSSVYVTPQNY-GVEQVBFYGVKGHIVYRGDKYD-----LTYDSDQLPPD--GE 445	

Qy	467	PLEKAYSHOLNAYAECFLMQD	--RRGTIPFFTMTHRSVDFPNTDAEKITOLPVVAYAL	523
Db	449	PIHRYXTHRLCHATAIFKSTPDYDNATIPIFSWTHRAEYNYRIYPNKITKIPAVKMYKL	508	
Qy	524	SSGGASIIIEPGPFCCGNLFLKESSNIAKFKYTLNSAALLORYVRIRYASTTNLRLFVQ	583	
Db	509	DDPSSTVVKSPGFTGCDLV-KRGSTGYGDIKATVNS-PLSQSKYVRVRYAT-----	557	
Qy	584	NSNNPFLTYIN-----KTMKNDLTYQFDLATNSNMGFSGDKNELLIG	630	
Db	558	NVSGGFNV-YINDKTLQTKFQNTVETGEGKDLTGSFGYIEYSTTQFDEHPKITHL	616	
Qy	631	AESFSVNEKLYIDKIEFIPVQL	652	
Db	617	LSDLSNNSSFYVDSSEFIPVVD	638	
RESULT 1				
Q9F0PB				
ID	Q9F0PB	PRELIMINARY;	PRT;	719 AA.
AC	Q9F0PB;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)		
DE	CRYLI.			
GN	Name=CRYLI;			
OS	Bacillus thuringiensis.			
OG	Plasmid pBCT19.			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			
OX	NCBI_TaxID=1428;			
RN	[1]			
RP	SEQUENCE FROM N_A.			
RC	SEQUIN-BTC0007;			
RX	MEDLINE=22837682; PubMed=12957903;			
RX	DOI=10.1128/AEM.69.5.5207-5211.2003;			
RA	Song P., Zhang J.J., Gu A., Wu Y., Han L., He K., Chen Z., Yao J.,			
RA	Hu Y., Li G., Huang D.,			
RT	Identification of cry1-type genes from <i>Bacillus thuringiensis</i> strains and characterization of a novel cry1-type gene.";			
RL	Appl. Environ. Microbiol. 69:5207-5211(2003).			
DR	EMBL: AF21119; AAG43526.1; -.			
DR	HSSP: P02965; ICTV.			
DR	GO:0005102; P:receptor binding; IEA.			
DR	GO:0006952; P:defense response; IEA.			
DR	GO:0009405; P:pathogenesis; IEA.			
DR	InterPro; IPR001178; Endotoxin.			
DR	InterPro; IPR005638; endotoxin_C.			
DR	InterPro; IPR005639; endotoxin_N.			
DR	InterPro; IPR008979; Gal_bind_Like.			
DR	Pfam; PF00394; Endotoxin_C; 1.			
DR	Pfam; PF00555; Endotoxin_M; 1.			
DR	Pfam; PF03945; Endotoxin_N; 1.			
KW	Plasmid.			
SQ	SEQUENCE	719 AA;	81024 MW;	7E17481922C435B6 CRC64;
Query	Match	32.8%	Score 1118.5;	DB 2;
Best	Local Similarity	37.3%	Pred. No. 1.3e-64;	Length 719;
Matches	253;	Conservative	130; Mismatches 235;	Indels 61; Gaps 17;
Qy	1	MNPNNRSEHDTI-----KVTNPSELQTNQHNOYPLADNPNSTLLEINYKEFLRMTEDSS	53	
Db	1	MKLNPKDQHSSNAKVDKIAADS-----LKVNEFLKINHEDFLRMSBES 50		
Qy	54	TEVLDNSTVTKDAVGTGIGSVVGVGVPFAGALSYFQSPLNTIWPSSADPMKAFMAQ	113	
Db	51	--IDPFVSIASITQGIGIAKGLTGLVPGFQIASLYSFGLGKTSWLFMEH 107		
Qy	114	VEVILDKKIEYAKSKAELQLOGIQQNFEDYVNALNSWKKTPLSLSKRSRSDRIRLFLFSQ	173	
Db	108	VEEIDQKISTYANIAIADLKGSDGALAVTHESLESWIK--NRNMRARATSVVSKSQYIA	164	
Qy	174	AESHERNSMSPFAWSKFEVLFPLTYAQAAANTHILLKDAVQFEGYSSSEDAVEFYHRQ	233	

Db	165 LELLFVQKLPSFAVSGEEVLLPPIYAQANLHLQQLRDAVSFGEKGWLINSQISTFVNQ	224	CC	EMBL; U04368; AAA21121.1;
Qy	234 LKLTOQYTHCIVNWNNGLRLRSSTYDWKENRERMTLTWDLIVLPPFDIYLRS 293		DR	DR HSSP; P07130; 1D1C;
Db	225 VERTSDYSHCVRKVSTGNNLRLCTNAESWVNQFRKMTLWVLDLALFPSTYDLYVPP 284		DR	InterPro; IPR01178; Endotoxin.
Qy	294 KGVKTEBLTIDP1F5INTLQEV-----GPTFUSLNS-IRKHFDFYLGTEF 343		DR	InterPro; IPR05638; endotoxin C.
Db	285 IKTISQLTREVYTDAGTHPNASFASTIYNNNAPSFAIESAVVRPHLDFLEQVTT 344		DR	InterPro; IPR08979; endotoxin N.
Qy	344 HTRLQPGYCFKDSFNYSGNYYVTRPSIGSSKTKITSPFYGDKSTEPVQKLSFQGKQYRT 403		DR	InterPro; IPR08944; Endotoxin C; 1.
Db	345 YSLIS-RWNSNTQNMWGGHLFR-TIGCVLNTSTQGSNTNSINPV-TLPFTSDYVTR 401		DR	PFam; PF00555; Endotoxin M; 1.
Qy	404 IANTDVAAPMPNGKYLGYTKVDFSOYDQKNETSTQYDSKRNGHVSAA---QDSIDQI 459		DR	PFam; PF03945; Endotoxin N; 1.
Db	402 ESLAGLNLFLTQPY-N-GVVRDPF---HVKFATPLIASPNFYYLGAGVGTQLODSENEL 456		KW	Sporulation; Toxin.
Qy	460 PPEETDEPPELEKAISHLQNLNAAECFLMQDRGTTIPPFWTWRSVDPFNTIDAEKITQLPVVK 519		SEQUENCE	1138 AA; 129658 MW; E12DC800CA56D1DA CRC64;
Db	457 PPETGQPNYESYSHRLSHIGLISASHVYALV--YSWTHRSARTNTLIEPNSTQIPLVK 514		Query Match	32.8%; Score 1117; DB 1; Length 1138;
Qy	520 AYALSSGASATIEGPGFTGGNLLFLKESSNSIAKEPKVTLNSAALLQYRVRIRYASTTNLR 579		Best Local Similarity	37.2%; Pred. No. 3; 2e-64;
Db	515 AFNLSSGAAVVRGPGTGGDIL-RRTNTGTFDIRVNIN-PPFAQRTYRVRIRYASTIDQ 572		Matches	253; Conservative 115; Mismatches 242; Indels 70; Gaps 19;
Db	580 LFVQ-----NSNNDFLYIYINKMNNKDDLTQTEFLAATTNSNMGFSGDNELIIGES 633		Qy	1 MNPNRNRSEHDHTIKVTPNSBLOTNHNQYPLADNPNSTLBELEYNKEFLRMTEDSSTEVLUDNS 60
Db	573 FHTSINGKAINQGN-----FSATMNRGDDYKTFRTYRGTFTPSFSDVQSTFTIGAWN 626		Db	1 MNLNNLNLGGYEDSNRNLNNSL-----NYTQKALSPSLKMNNTQDFLSITEREPEALASG 55
Qy	634 FVSNEKIIYDKEKIEFIPVQL 652		Qy	61 TVRDAVGRG1SIVGQVLGVGVPFGAGALTSPYQSFSLNTIWPSSADPKWPKAFMAQEVLDK 120
Db	627 FSSGENEVYDRIEFVVPVVE 645		Db	56 NT---AINTVVSYTGTALSALGVPGASAFITNFVYLKITGILWPHDKNINDEFMTETVETLIEQ 113
RESULT 18			Qy	121 KIBYAKRSKRALABQGLONNFEDYVNAINSWKTPSLRSRSQRDRBLFSOASHERN 180
C7AB_BACUK	STANDARD;	PRT; 1138 AA.	Db	114 KIEOYARNKALAELEGGLNNLTYQQALEDWLNNP---DDPATITRIVDFFRFLDALES 170
ID_C7AB_BACUK			Qy	181 SMPSFAVSKFEEVLFPLPTYAQAAANTHLLLKDQYFGEWGSSEDAEFYHROLKLTQY 240
045708;			Db	171 YMSFSFRVAYEIPLLTYAQAANLHALLRDRSTLYGDKWBTIONNIEENYNRKHSIBY 230
045708;			Qy	241 TDHICVNTNNGLNRSTYDAMKVNFRERMTLTIVLFLIVLFPFDIRLYSKGVVTEL 300
16-OCT-2001 (Rel. 40, Created)			Db	231 SNEHCVKYVNSGLSRLNGSTYEQWINTNRFRERMTLWVLDIAAVFPVYDPRMYSMETISIOL 290
16-OCT-2001 (Rel. 40, Last sequence update)			Qy	301 TRDIFTDPIFSINTLQEYNGPTFUSIEN-SIREKHLFDYLOGIEFPT-----RLQPOY 351
05-JUL-2004 (Rel. 44, Last annotation update)			Db	291 TREVYDPIISLTSISNPQGIPGSFSQMENIAIRPHLVDLYEITYSKYKAFSHIQPDLL 350
DB_Pesticidial crystal protein cry7Ab (Insecticidal delta-endotoxin CRYVIIAb) (Crysaline entomocidal protein) (130 kDa crystal protein)			Qy	352 FGKDSFNYWSGNYVETRPSIGSSKTTSPFYGDKSSTEPMVQK--LSFDGQKVYRTIANTDV 409
DE			Db	351 F-----YWSAHKVSPKQS-EQSNLTYIGY-KTSGYISSGAYSFRGNDIIRTLaAPS 402
DE			Qy	410 AAWPGKVLGYLGYDQDKNEITSQYDTSKRNNGHVSQADSIDQLPPETTDEPLIE 469
DE			Db	403 VVYPTQNY-GVEQFVYGVKGVHRYGDNKYD-----LTYDSDIDQLPP--GEPHT 451
DE			Qy	470 KAYSHQLYNAECPLMDD--RRGTIPPFETWRSVDFNTIDAEKITOPPVVKAYAALSG 526
DE			Db	452 EKYTHRLCHATATSKTPDYDNTAPIFSWTHRSVAYNRIIPNKTIPKIPAVKMYKLGDT 511
SEQUENCE FROM N.A.			Qy	527 ASIIEGPGFTGGNLLFLKESSNS-IAKFKVTLNSAALLQYRVRIRYASTTNLRFVONS 585
RC			Db	512 STVVKGPQFTGDL--VRGSGNYIGDIKATVNS-PLSQNYRVRIRAT-----NV 559
STRAIN=ID867;			Qy	586 NNDFLVYIN-----KTMKQDDDTYQTFPLATINNMGFSGDKRNELIGAE 632
RC			Db	560 SGQENV-YINDKILQRKFQNTVETGKGDLTYGSGFYEYSTTQPDKHPKTRTHLS 618
Payne J.M., Fu J.M.;			Qy	633 SFTSNEKIIYDKEFIPVQL 652
"Cooperative active Bacillus thuringiensis isolates and genes encoding epithelial cells of Coleoptera.			Db	619 DLSSNNSSPFYVDS1STEFIPVVD 638
Patent number US586488, 15-FEB-1994.			RESULT 19	
CC -1- FUNCTION: Promotes colloidosmotic lysis by binding to the midgut epithelial cells of Coleoptera.			CID_BACLU	
CC -1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.			ID_CID_BACTU	STANDARD; PRT; 719 AA.
CC -1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.			AC_Q9XDL1;	
CC -1- SIMILARITY: Belongs to the delta endotoxin family.			DT_16-OCT-2001 (Rel. 40, Created)	
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			DT_16-OCT-2001 (Rel. 40, Last sequence update)	
CC			DT_05-JUL-2004 (Rel. 44, Last annotation update)	

DE	Pesticidial crystal protein cryII (Insecticidal delta-endotoxin CryII (d)) (Crystaline entomocidal protoxin) (81 kDa crystal protein).
DE	NAME=cryII (d); Synonyms=cryII (d), NRcRYV;
OS	Bacillus thuringiensis.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX	NCBI TaxID:1428;
RN	SEQUENCE FROM N.A.
RP	SEQUENCE N.A.
STRAIN=B90;	
RC	
RX	Medline=20374042; PubMed=10919402;
RA	Choi S.-K., Shin B.-J., Kong H.-M., Park S.-H.; "Cloning of a new Bacillus thuringiensis cryII-type crystal protein gene."; Curr. Microbiol. 41:65-69 (2000).
RT	Curc. FUNCTION: Promotes colloidiosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae. Active on Plutella xylostella and on Bombyx mori.
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; AF047579; AAD44366.1; -.
DR	HSSP; P02965; 1C1Y.
DR	InterPro; IPR001178; Endotoxin.
DR	InterPro; IPR005638; endotoxin_C.
DR	InterPro; IPR008979; Gal_bind_like.
DR	PFAM; PF03944; Endotoxin_C_1.
DR	PFAM; PF00555; Endotoxin_M_1.
DR	PFAM; PF03945; Endotoxin_N_1.
KW	sporulation; Toxin.
SQ	SEQUENCE 719 AA; 81403 MW; F335F589D3B0C45 CRC64;
Query Match	32.8%; Score 1115.5; DB 1; Length 719;
Best Local Similarity	37.8%; Pred. No. 2.le-64;
Matches	253; Conservative 123; Mismatches 225; Indels 69; Gaps 18;
DB	PLADNPNTSLEELNKFRIMTDSSTE VLDNSTKDAV 66
Qy	NHQQY-----PLADNPNTSLEELNKFRIMTDSSTE VLDNSTKDAV 66
DB	5 NQNMYSFESSNATWDKSFTDPLENTNMEQLNSNHEDCLKMSYESEVPEVSYSTIQ--- 61
Qy	67 GIGTSVGVGQI LGVGPPFAGALTSFYQSFNLTWPSDADWKAFMAQEVFLDKKIEVA 126
DB	62 -TGIGAIGLIGNQVPAQVQVAVLSPFQKGSQWEIHEVFLKLKISYA 120
Qy	127 KSKKALAEQLOGQNNPFDYTNALNSWKKTPISLRSKRSQDIREU---FSQAESHFNRNM 182
DB	121 RNKALADLQKDALAVTHESLWIE----NRNNTRVRSLPSKQVTALEMFMVQKL 173
Qy	183 PGPVSKPKEFPLTQYAQANTHLLKIQKQVEGPGYSSVEDAEFYHQQLKUTQYD 242
DB	174 PSFAVSGEVEPLPPLPQYQANLHLLRDLRASIFKEWGLSEESTFYNQROSSQREYSD 233
Qy	243 HCVWVWYNGLNGLRGSTDWNKVNFRREMTLTLVLFPPDYLXSKGKTELTR 302
DB	234 YCSWVWYNTQNLGRPCTNAEWSWRQNQFRMTMVLMLVLFPSDTRAYPIPTSAQLR 293
Qy	303 DIFTDPFISLNTDLEY-----GPTFLEIENS-IRKHLFDYDLYGTFHTRLQPGYF 352
DB	294 EYVTDAGTWHPNASFASTTWNNAFPSTTIEAVVRNHLDFLEQVITYSLLS-RNS 352
Qy	353 GKDSENYWGSNYVTRPSIGSSK7K1SPFQDKSSTEPVQQLSFDGQKVTNTDVAW 412
DR	BMBL; U04367; AA21120.1; -.
DR	HSSP; P07130; 1DLC.
DR	InterPro; IPR001178; Endotoxin.
DR	InterPro; IPR05638; endotoxin_C.
DR	InterPro; IPR05639; endotoxin_N.
DR	InterPro; IPR08979; Gal_bind_like.
DR	PFAM; PF03944; Endotoxin_C_1.
DR	PFAM; PF00555; Endotoxin_M_1.
DR	PFAM; PF03945; Endotoxin_N_1.
KW	Toxin.
SEQUENCE	1138 AA; 129778 MW; 01DF7072C074CE88 CRC64;
SQ	

Query Match	Score	Length	DB	1	Best Local Similarity	Score	1112;	Length	1138;
Matches	248;	Conservative	124;	Missmatches	244;	Indels	58;	Gaps	19;
1	MNPINRSEHDITKTPNSLQTNINQYPLADNPNSTLLEBNYKEFLRNTEDSSTEVLQNS	60							
1	MNUNLGGEDSNTLNSL-----NYPQTQKALSPSLKMMYQDFDLSTTERQEPAELLS	55							
61	TVDAVGTSIISWVQILGVGVPPAGASLFSYQSFLLNTIWPSPADPWFKAQVEVLIDK	120							
56	NT-AINTVUSVTGATLSSLGVPGASLFINVYKIGLWPHANKNIDWDEFMTETLIDQ	113							
121	KIEFYAKSKAELQGLQNNFEDYNAWNWKTPSLRSKRSQDIRELFSQAESHRN	180							
114	KIEQYARNKAELAEGLGNNLITYQQALEDWLNNP---DDPAPITTRVDRFRFLDAPES	170							
181	SMPSFAVSKPEVLEPLPTIAQAAANTHLLLKAQVFLNPFGEENYSSDVAEPYHRLKLTQY	240							
171	YMPFRRVAYEIPPLTVYAAQANLHLALLRDSTLYGDKKGFTQNONIEENYRQKXHSEY	230							
241	TDHCVNWTNVGLNLRGTSYDAWKFNFRFREMTLTVLDLVLFFFYDILYSGKVTTEL	300							
231	SNHCVKWNGLSLRNGSTYEQWINYNNFRFREMLMVIDIAAVFPIYDPRMSTMSITQQL	290							
301	TRDIFTDPFLSLNTLQEQYGPTELSIEN-SIRKPHFLDQYQIEFH-----RLQGQY	351							
291	TREYTDPSLSSNPDGPSFSGMENATAFRTPHLVDLDELYIYTSKYKAFSHIEIQDPL	350							
352	FGDTSFNVWSGNYVETRPIGSSKTTSFYGDKSTEPVQK--LSFDGQKVYRTIANTDV	409							
351	F----YMCVHRYVSFKKS-EQSNLYTIGIY-KTSGYISSGAYSFRGNDIIRTLLAAPSIV	402							
410	AAWPNGKTYLGLTIVKVDFSQYDQKNETSTQYDLSKRNNGHVSQDSDIDQLPPTTDEPLE	469							
403	VVPPYQTQY-GVPEQYFCKVGHYHGDNKYD-----LTYSDIDQLPPD-GEEIH	451							
470	KAYSHQLNAYAECFLMQD---RRGTIPFFTWTHRSVDFPNTIADEK1TOLPVVKAAYA1SSG	526							
452	EKYTHRLLCHATAISKSTPDPYDNATIPIPSWTHRSAEYNNRYIINKIKIPAVKMYKLDL	511							
527	ASLIEGPGETGGNLLFLKESNS-IAKEPKVTLNSAALLQYRVRIRYASTTN--LRLFVQ	583							
512	STVVKGPGETGGD--VVRGSGNYIGDIKATVNS-PLSQYKVRVRATSVSCLNFVFI-	567							
584	NSNNDDFLVYIN----KIMNNKDDDTYOTFELATTSNMGFSGDKNELLIGAESFSVNE	638							
568	--NDEIAQKNFQSTVETIGERDLTYSGYTEYSTTIOPPNHEPPKTTULNLHNSNN	624							
639	KIYIDKIEFIPVQL	652							
625	PFVYDSIEFIPVVD	638							

PT	VARIANT	233	233	D -> Y (in strain JHC4835 and strain HD-1).	RA	Song F., Zhang J., Gu A., Huang D., Li G.; Submitted to EMBL/GenBank/DBJ databases.
PT	VARIANT	443	443	A -> V (in strain AB88).	RL	
PT	VARIANT	711	712	KQ -> NE (in strain HD-1 and strain 61).	DR	
PT	SEQUENCE	719 AA;	81216 MW;	3627E5A6C25DAFF5 CRC64;	DR	HSSP; P09965; 1.CY.
Query Match	Best Local Similarity	32.3%	Score 1100.5; DB 1; Length 719;	DR	GO: 0005102; F: receptor binding; IEA.	
Matches	249;	Conservative	317; Mismatches 231; Indels 63; Gaps 19;	DR	GO: 0006952; P: defense response; IEA.	
Qy	1	MNPNNRSEHDTI-----KVTPNSELQTNHQYPLADNPNSTLEELNKFRLRMTEDSS 53	DR	GO: 000905; P: pathogenesis; IEA.		
Db	1	MKLKNQDKHQSSNNAVKD1KSTD-----LGNEDIELONINHEDCLMSEYEN 50	DR	InterPro: IPR001175; Endotoxin.		
Qy	54	TE-VLDNSTVDAVNGCISVQQLGVGVPRFAGALTSPYQSEFNTWPLSDADPKAFMA 112	DR	InterPro: IPR05638; endotoxin C.		
Db	51	VEPFVSASTIQ---TGIGIACKLGLTGVPAQYASLSPFILGPWPKKNQWEIIME 106	DR	InterPro: IPR05639; endotoxin N.		
Qy	113	QVEVLIDKRIJEPYAKSKAALAEIQLQNLNFEDVNAWSKTPPLSRSKSDQRRELFS 172	DR	InterPro; IPR08979; Gal bind Like.		
Db	164	AELMFTQKLPSFAVSCBEEVPLPILYPAQANHLILRDAISFGREWGLSSSEISTFYNR 223	DR	Pfam: PF003944; Endotoxin C; 1.		
Qy	233	QKLQTQYTDHCVNNWVNGVNLGLRGSYSTDAYNKVKENFERRENTLTVLDLTVLFPEFDIRLY 292	DR	Pfam: PF003945; Endotoxin N; 1.		
Db	224	QAESHFNRNIMPFAVSKPEVFLPITYAQANTHLLIKDQAOFGEWGYSSSEDAEFYHR 232	DR	SEQUENCE 719 AA; C629DFC44827241 CRC64;		
Qy	293	SKGVKTBPLTRDIFTD-----PIFSLNT-LQEXQPTFESIENS-IRKPHFLDYLOGIE 342	DR	Query Match 32.3%; Score 1100.5; DB 2; Length 719;		
Db	284	PIKTTAQIQTREYVTDAGTVHHPHPSFSTTAWYNNNHPSSATEAAVYRNPHLLDPLFQVT 343	DR	Best Local Similarity 36.6%; Pred. No. 2e-63; No. 2e-63; Gaps 19;		
Qy	343	FHTRLQPGYFGKDSFVNWSGNVYVETRPSKTSRPSKTSFQKLSDQGKVR 402	DR	Matches 249; Conservative 137; Mismatches 231; Indels 63; Gaps 19;		
Db	344	IYSLLS-RWSNTQYNNMNGKHLERF-TIGGTLNISTQGNTNTSINPV-TLPFTSRDVYR 400	DR			
Qy	403	TIANTDVAAWPNQKVKYLVGTVKDFQDQKNETSTQYDSKRNNGH---VSAOPSDIQ 458	DR			
Db	401	TESLAGLNLFU-TQPVN-GVPRDF---HWFVFTHPLASDNFYYPGAGGTQLODSENE 455	DR			
Qy	459	LPPETDEPLEKAYSHOLNAYABCEFLMQDRGRTIPFFTWHSVDFENTIADKEKITQLPVY 518	DR			
Db	456	LPPEATCOPYTESYSHRLSHIGLISASHVAKLV-YSWTHRSADRNTTIEPNNSITOIPLY 513	DR			
Qy	519	KAYALSSGASILBGPGETGNLFLKESNSNIAKFTYTLNSAALLORYRIRYASTTNL 578	DR			
Db	514	KAFNLSSGAAVVRGPGETGFDLIL-RRTNTGTFGDIRVNIN-PPFAQRYRIRYASTTDL 571	DR			
Qy	579	RLFVQ---NSNNDFLIVYIYNTKWNKDDLTYQFDLATTNSNGFSGDRKNELLIGAE 632	DR			
Db	572	QPHTSINGKAINQGN---FSATMNRGEGLDLYKTFRTVGETTPFSFLDVQSTFTIGAN 625	DR			
Qy	633	SPVSNEKXYIYDKEFIPVQL 652	DR			
Db	626	NTSSGNERYVDRFVPUV 645	DR			
Qy	634	RESULT 22	DR			
AC	Q93NJS	PRELIMINARY;	DR			
AC	Q93NJS;		DR			
ID	01-DEC-2001	(TREMBLrel. 19, Created)	DR			
DT	01-DEC-2001	(TREMBLrel. 10, Last sequence update)	DR			
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)	DR			
DE	Cry1Ia.		DE			
GN	Name=cry1Ia;		GN			
OS	Bacillus thuringiensis.		OS			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		OC			
OX	NCBI_TaxID=1428;		OX			
RN	[1]		RN			
RP	SEQUENCE FROM N.A.		RP			
RESULT	23		RESULT			
Q6X181	PRELIMINARY;	PRT;	Q6X181	PRT;		
ID			Q6X181			
AC			AC			
633	SFVSNEKXYIYDKEFIPVQL 652		633			
626	NTSSGNERYVDRFVPUV 645		626			
579	QPHTSINGKAINQGN---FSATMNRGEGLDLYKTFRTVGETTPFSFLDVQSTFTIGAN 625		579			
514	KAFNLSSGAAVVRGPGETGFDLIL-RRTNTGTFGDIRVNIN-PPFAQRYRIRYASTTDL 571		514			
519	RESULT 23		519			
572	QPHTSINGKAINQGN---FSATMNRGEGLDLYKTFRTVGETTPFSFLDVQSTFTIGAN 625		572			
519	KAYALSSGASILBGPGETGNLFLKESNSNIAKFTYTLNSAALLORYRIRYASTTNL 578		519			
514	KAFNLSSGAAVVRGPGETGFDLIL-RRTNTGTFGDIRVNIN-PPFAQRYRIRYASTTDL 571		514			
579	RLFVQ---NSNNDFLIVYIYNTKWNKDDLTYQFDLATTNSNGFSGDRKNELLIGAE 632		579			
572	QPHTSINGKAINQGN---FSATMNRGEGLDLYKTFRTVGETTPFSFLDVQSTFTIGAN 625		572			
514	KAFNLSSGAAVVRGPGETGFDLIL-RRTNTGTFGDIRVNIN-PPFAQRYRIRYASTTDL 571		514			
519	RESULT 23		519			
Q6X181	PRELIMINARY;	PRT;	Q6X181	PRT;		
ID			ID			
AC			AC			
633	SFVSNEKXYIYDKEFIPVQL 652		633			
626	NTSSGNERYVDRFVPUV 645		626			
579	QPHTSINGKAINQGN---FSATMNRGEGLDLYKTFRTVGETTPFSFLDVQSTFTIGAN 625		579			
514	KAFNLSSGAAVVRGPGETGFDLIL-RRTNTGTFGDIRVNIN-PPFAQRYRIRYASTTDL 571		514			
519	RESULT 23		519			
Q6X181	PRELIMINARY;	PRT;	Q6X181	PRT;		
ID			ID			
AC			AC			

DT	05-JUL-2004	(TREMBLrel. 27, Created)	Qy	633 SFVSNKEKIVIDKIEFIPVQL 652
DT	05-JUL-2004	(TREMBLrel. 27, Last sequence update)	Db	626 NFFSGNEVYDIREVPUVEV 645
DE				
GN				
GN	Bacillus thuringiensis	Bacillales; Bacillaceae; Bacillus.	RESULT 24	
OC			Q8KY61	PRELIMINARY;
OX	NCBI_TaxID=1426;		ID	
RN	[1]		AC	Q8KY61;
RP	SEQUENCE FROM N.A.		DT	01-OCT-2002 (TREMBLrel. 22, Created)
RA	Espindola R., Lemos M.V.P., Lemos B.G.M., Sena J.A.D.;		DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
RL	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.		DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
EMBL	AY62167; AAP86782.1; -		DB	
DR	GO:000102; F:receptor binding; IEA.		OS	Bacillus thuringiensis
DR	GO:0006952; P:defense response; IEA.		OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	GO:0009405; P:pathogenesis; IEA.		OC	NCBI_TaxID=1428;
DR	InterPro; IPR01178; Endotoxin.		RN	[1]
DR	InterPro; IPR005638; endotoxin_C.		RP	SEQUENCE FROM N.A.
DR	InterPro; IPR005639; endotoxin_N.		RA	Porcar M., Martinez C., Caballero P.;
DR	InterPro; IPR008979; Gal_bind_Like.		RA	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR	Pfam; PF03944; Endotoxin_1.		DR	EMBL; A227877; AAC73516.1; -
DR	Pfam; PF00555; Endotoxin_M.		DR	PIR; B42459; B42459.
DR	Pfam; PF01945; Endotoxin_N.		DR	HSSP; P02965; 1C1Y.
SQ	SEQUENCE 719 AA; 81216 MW; 3627E5A6C25DAFF5	CRC64;	DR	GO:0005102; F:receptor binding; IEA.
Qy	Query Match 32.3%; Score 1100.5; DB 2; Length 719;		DR	GO:0006932; P:defense response; IEA.
Matches 249; Best Local Similarity 36.6%; Pred. No. 2e-63; Gaps 19;			DR	InterPro; IPR01178; Endotoxin.
Qy	1 MNPNRSEHDITI-----KVTPNSELQTNHNOYPLADNPNSTLELNKFRLRMTEDS 53		DR	InterPro; IPR005639; endotoxin_N.
Db	1 MKLKNQDQHOSPFSSNAVKDKISTDS-----LKNETDIELQNINHBDCLRKSEYEN 50		DR	InterPro; IPR008979; Gal_bind_Like.
Qy	54 TE-VLDNSTVKAQVTKDAGTGIISVQGQLGVVCPPEAGALTYSQSFUNTINWSDAPWKAFM 112		DR	Pfam; PF03444; Endotoxin_C; 1.
Db	51 VEPPVASTIQ---TGIIGAKIGKLTGTVPEAGAVSLSYFELGELWPKGNQWELME 106		DR	Pfam; PF00555; Endotoxin_M; 1.
Qy	113 QVEVLDKKEBEYAKSKAALBQALQNNFEDYNALNSKTKPLSLRSRSQDIRELTS 172		DR	PF03945; Endotoxin_N; 1.
Db	107 HVEEINQKISTYARNKALTDLKIGDAAVYHOSLESWVG--NRNTRNTRASVTKSQYI 163		SQ	SEQUENCE 719 AA; 80984 MW; 84F128724626473 CRC64;
Qy	173 QAESHHFRNNSMPSFAVSKFEYLFLPTYAQANTHILLKDAQVFGEEWGYSSEDVAEYHR 232		Qy	1 MNPNRSEHDITI-----KVTPNSELQTNHNOYPLADNPNSTLELNKFRLRMTEDS 53
Db	164 ALELMFVQKLPSFAVSGEEVPLPYIAQANHLILLRDASIFGEWGLSSB1STFYN 223		Db	1 MKLKNQDQHOSPFSSNAVKDKISTDS-----LKNETDIELQNINHEDCLKISEYEN 50
Qy	233 QKLUTQQYTDHCYVNWYNGLNGLRGSTDYAWKVNRFREMTLTVDLIVLFFDYLRY 292		Qy	54 TE-VLDNSTVKAQVTKDAGTGIISVQGQLGVVCPPEAGALTYSQSFUNTINWSDAPWKAFM 112
Db	224 OVERGADWSYDCHVCKYSTGLNLRGSTDYAWKVNRFREMTLTVDLIVLFFDYLRY 293		Db	51 VEPPVASTIQ---TGIIGAKIGKLTGTVPEAGAVSLSYFELGELWPKGNQWELME 106
Qy	293 SKGVKTELDRDIFT-----PIFSLNT-LQEXGPFLSLENS-IRKPHEDYLOGTE 342		Qy	113 QVEVLDKKEBEYAKSKAALBQALQNNFEDYNALNSKTKPLSLRSRSQDIRELTS 172
Db	284 PIKTTAQLTREVYTAIGTVPHPHESFTSTWYNNNAPSSAEEAVRNPFLDFFQV 343		Db	107 HVERINQKISTYARNKALTDLKIGDAAVYHOSLESWVG--NRNTRNTRASVTKSQYI 163
Qy	343 FHTRLQPGYFGKDSFNWGNVYETRPSIGSKTITSPPYGDKSTEYQKLSPDQKQYR 402		Qy	224 OVERGADWSYDCHVCKYSTGLNLRGSTDYAWKVNRFREMTLTVDLIVLFFDYLRY 292
Db	344 IYSLIS-RWSNTQYMMWGHKLERF-TIGGMLNTSQTNTNTSINPV-TLPFTSRDVR 400		Db	224 PIKTTAQLTREVYTAIGTVPHPHESFTSTWYNNNAPSSAEEAVRNPFLDFFQV 343
Qy	403 TIANTDVAWPNKGKVLYGTVKDPQYDQKNETSTOTVDSKRNGH---VSAQDSIDQ 458		Qy	293 SKGVKTELDRDIFT-----PIFSLNTLQEXY-----GPTFLSLENS-IRKPHEDYLOGTE 342
Db	401 TESLAGLNFLTQPVN-GPVRVDF----HMKWFTTHPIASDNFTYPGYAGIGTQDQDSENE 455		Db	343 FHTRLQPGYFGKDSFNWGNVYETRPSIGSKTITSPPYGDKSTEYQKLSPDQKQYR 402
Qy	459 LPPTTDEPLEKAYSHQMLTAECFLMQDERRGTTIPFPTWTHRSYDFFNTDAEKITQLPV 518		Qy	344 IVSLLS-RWSNTQYMMWGHKLERF-TIGGMLNTSQTNTNTSINPV-TLPFTSRDVR 400
Db	456 LPPTTDEPLEKAYSHQMLTAECFLMQDERRGTTIPFPTWTHRSYDFFNTDAEKITQLPV 513		Db	403 TIANTDVAWPNKGKVLYGTVKDPQYDQKNETSTOTVDSKRNGH---VSAQDSIDQ 458
Qy	519 KAYLSSGASLIEGGFTGNLFLPKESSNSIAKPKVTLNSAALLQYRVRYASTNTL 578		Qy	401 TESLAGLNFLTQPVN-GPVRVDF----HMKWFTTHPIASDNFTYPGYAGIGTQDQDSENE 455
Db	514 KAFNLSGGAAVVRGPFTGFTGDL-RRTNTGTFDIRVNNN-PPFAQRYRVRYASTTD 571		Db	459 LPPTTDEPLEKAYSHQMLTAECFLMQDERRGTTIPFPTWTHRSYDFFNTDAEKITQLPV 518
Qy	579 RLFTQ-----NSNNDFLVYIYNTMNNKDDLYTQFELATTNSNMGSGDKNELIGAE 632			
Db	572 QFHTSINGRAINQGN-----FSATMNRGEBDLDPYQSTFTGICW 625			

Db	456	LPETTCQPNYESYSHRLSHIGLISASHVAKLV-- YSWTHRSADRTNTIBPNSITQIPLV	513	Db	284	PIKTTAQLTREVYTAIGTVPHBFSFTSTIWNNAAPSAIEAVRNPHLDFLEQVT	343	
Qy	519	KAYALSGGASLIEGPGTGTGNNLFLKMESSNSIAKFCVTLNSAIIQLQYRIRYASTNTU	578	Qy	343	FHTRIQLQGYFGKDSFNYSGNYVETRSPFGSSKTTISPFYGDKESTEPIQKLSPGQKXVR	402	
Qy	514	KAFNLSSGAAVVRGPGTGGDL-L-RTNTGTFGDLRVNIN-PPFAQRYRIRYASTNTD	571	Db	344	IYSLIS-RWSNTQYMMWGGHKLFR-TIGGTLNISTSGTNTSPN-TPFETSRDV	400	
Qy	579	RLFVQ----NSNNNDPLVYIINKTNKNDDDIYQPTDLATINSNGNGSDRNELLIGAE	632	Qy	403	TIANTDVAAMPNGKYLGVTKDFEQYDDQKNETSTQTYDSKRANGH---VSQDSDIQ	458	
Db	572	QPHTSINGKANQGN----FSATMNRGEBDLYDRTPTVGETPPSFVQSTFTIGW	625	Qy	459	LPPETTDEPLEKAYSHQLNAYAECFLMDQRGTTIPFPTWTRSYDFFNTDAEKITQLPVV	518	
Qy	633	SFVSNEKLYIDKIEFIPVQL	652	Db	401	TESLAGLNLLTQTPN-GVPRVDF-- -HWKFVTHPIASDNFYYFYGAGTQLOQDSENE	455	
Db	626	NFSSGNEVYIDRIEFVVEV	645	Db	456	LPPEATGQPNEYSSYRSLSHIGLISASHVAKLV-- YSWTHRSADFTNTIEPNSTQIPLV	513	
<hr/>								
RESULT 25								
Qy	805796	PRELIMINARY;	PRT;	719 AA.	Qy	519	KAYALSGGASLIEGPGTGTGNNLFLKMESSNSIAKFCVTLNSAIIQLQYRIRYASTNTL	578
AC	085796;				Qy	514	KAFNLSSGAAVVRGPGTGGDL-RRTNTGTFGDLR-RTNTGTFGDLR-RTNTGTFGDLR	571
DT	01-NOV-1998	(TrEMBLref)	08	Created)	Db	579	RLFVQ----NSNNDFLVYIINKTMNDDDLTVQFDLATNSMGFSDKNEELIGAE	632
DT	01-NOV-1998	(TrEMBLref)	08	Last sequence update)	Db	572	QFHTSINGKAINQGN----FSATMNRGEBDLYDRTPTVGETPPSFVQSTFTIGW	625
DT	01-MAR-2004	(TrEMBLref)	26	Last annotation update)	Qy	633	SFVSNEKLYIDKIEFIPVQL	652
GN	Name-cry101;				Qy	626	NFSSGNEVYIDRIEFVPEV	645
OS	Bacillus thuringiensis	(subsp. kurstaki).			Db			
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				RESULT 26			
OX	NCBI_TaxID:29333;				C1BA_BACTK	C1BA_BACTK	STANDARD;	PRT;
RN	[1]				ID	C1BA_BACTK		1228 AA.
RP	SEQUENCE FROM N.A.				AC	P05571;	Q45731;	
RC	STRAIN=S10;				DT	05-NOV-1988	(Ref. 09, Created)	
RL	Zhong Q., Deng R., Long Q., Yuan M., Pang Y., Wang X.;				DT	01-FEB-1996	(Ref. 33, Last sequence update)	
DR	Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.				DT	05-JUL-2004	(Ref. 44, Last annotation update)	
DR	EMLB: AF076953; AAC2910.1; -				DE	Pesticidal crystal protein cry1Ba (Insecticidal delta-endotoxin protein).		
DR	HSSP: P02965; 1C1Y				DB	Cry1Ba) (Crystalline entomocidal protoxin) (140 kDa crystal protein).		
DR	GO: GO:0005102; F: receptor binding; IEA.				GN	Name-cry1Ba; Synonyms=cryA4, cryIBa;		
DR	GO: GO:0006952; P: defense response; IEA.				OS	Bacillus thuringiensis (subsp. kurstaki), and		
DR	GO: GO:0009405; P: pathogenesis; IEA.				OS	Bacillus thuringiensis (subsp. entomocidus).		
DR	InterPro: IPR001178; Endotoxin.				OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
DR	InterPro: IPR005638; endotoxin.				OC	NCBI_TaxID:29339, 1436;		
DR	InterPro: IPR0008979; Gal bind_Like.				RN	[1]		
DR	PFam: PF03944; Endotoxin_C; 1.				RP	SEQUENCE FROM N.A.		
DR	PFam: PF03945; Endotoxin_N; 1.				RC	SEQUENCES=B.t.kurstaki; STRAIN=HD-2;		
DR	Plasmid.				RX	MEDLINE=83203216; PubMed=3367680;		
KW	SEQUENCE 719 AA;	81230 MW;	42746D478359BBA7 CRC64;		RA	Brizard B.L., Whiteley H.R.,		
SQ	Query MatchScore 32.1%;	Score 1094.5;	DB 2;	Length 719;	RT	"Nucleotide sequence of an additional crystal protein gene cloned from		
Qy	Best Local Similarity 36.5%;	Pred. No. 5e-63;	Indels 63;	Gaps 19;	RT	Bacillus thuringiensis subsp. thuringiensis.";		
Matches	248; Conservative 137;	Mismatches 232;	Indels 63;	Gaps 19;	RN	[2]		
Qy	1 MNPNNRSEHTI-----KTPNSELOTNHNOYPLADNPNSTLEELNYKEPLMTDSS	53			RP	SEQUENCE FROM N.A.		
Db	1 MQLKNDQKHSQSSNAVKDQKISD-----LKNETDIELQNINHEDCLKMSBEYN	50			RC	MEDLINE=83203216; PubMed=3367680;		
Qy	54 TE-VLDNSTVKDAGTGISVVGQILGVGVPPFAGALTTSFYQSFNLTWPSDADPKAFMA	112			RA	Soeterart P.;		
Db	51 VEPFVASTIQ---TGIIGAKILGILGVPPFAGQVAVSILPSILGEWPKGKNOWEIME	106			RL	Brizard B.L., Whiteley H.R.,		
Qy	113 QVEVLIDKIEEYAKSVALAELQGLQNNFEDYNAALNSWKTPPLSLRSKRSODRILFSS	172			CC	"Nucleotide sequence of an additional crystal protein gene cloned from		
Db	107 HYBEIIINQISTYARNKALTDIKGLDIALAVYDLSLAWVG--NRNTRARSVSKYI	163			CC	Best Local Similarity 36.5%;		
Qy	173 QAESHPNMSPPASVSKPKEVLELPYTAQANTHLLKDAQVFGEEGNGSSEDVAFYHR	232			CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-		
Db	164 ALFLMFYQKLPSPPASVGEVPLPPIYQAQANLHLLRDAISLGKEWGLSSSEISFYNR	223			CC	the European Bioinformatics Institute. There are no restrictions on its		
Qy	233 QKLTKQTIDHCYNYWNGLNGLRGSTDAWYKFNRFERMLTVLVDLIVLPPFYDIRY	292			CC	use by non-profit institutions as long as its content is in no way		
Db	224 OVERAGDYSDHCKWYKSTGLNLRGTRNDESWTRYNQFRDMTLMVLDLVALFPSYDQMY	283			CC	modified and this statement is not removed. Usage by and for commercial		
Qy	293 SKGVKTELTRDIFT-----PIFSLNT-LQEGYPTFLSIENS-IRKPHLFQDLYGIE	342			CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/) or send an email to licensee@isb-sib.ch).		

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/>) or send an email to licensee@isb-sib.ch).

EMBL: X06711; CRA29898.1; -.

DR	EMBL; X95704; CAA65003.1; -.	DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
PIR	S00873; S00873.	DB	Cry1Ba.
DR	HSSP; P07130; 1DLC.	GN	Name=Cry1Ba.
InterPro	IPR001118; Endotoxin.	OS	Bacillus thuringiensis.
InterPro	IPR005638; endotoxin_C.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
InterPro	IPR005639; endotoxin_N.	NCBI_TaxID	1428.
InterPro	IPR008939; Gal_bind_Like.	[1]	
PFam	PF03944; Endotoxin_C.	RN	
PFam	PF00555; Endotoxin_M.	RP	SEQUENCE FROM N.A.
DR	PFam; PF03945; Endotoxin_N.	RA	Zhang J., Song F., Huang D.,
DR	SPorulation; Toxin.	RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
VARIANT	150 150 Y -> H (in strain HD-110).	DR	EMBL; AR368257; AAK6351.1; -.
FT	SEQUENCE 1228 AA; 139647 MW; C8E3A19FB3D98575 CRC64;	DR	HSSE; P07130; 1DLC.
SQ	Best Local Similarity 31.5%; Score 1072.5; DB 1; Length 1228; Matches 246; Conservative 120; Mismatches 247; Indels 59; Gaps 19;	DR	GO:0005402; F:receptor binding; IEA.
Query	1 MNPNRNRSEHDTRIKVTPNSLQTNTNQYPLADNPNSTLBEIINYKEFLRMTEDSSTEVIDNS	DR	GO:0005405; P:defense response; IEA.
Db	1 MTSRKNEENIINAVSNHSAQMD-----LLPARDIESLCLAEAGNN---IDPQ 45	DR	P:pathogenesis; IEA.
Query	611 TVKDAVGTCISVQGILGVGVPAGALTSPYQSFPLNTIWPSPADPKAFMAQVEVLIDK 120	DR	PFam; PF03944; Endotoxin_C.
Db	46 VSASTVQGTQINIAGRILGVGVPAGQLAQSFSPYLGEMWPRGRDQWTFLEHVEQLINQ 105	DR	PFam; PF00555; Endotoxin_M.
Query	121 KIEEYAKS KALAELQGLQNLQNFEDYVNAIWSKCKTPLSLRSKRSQDRIRE-LFSQL--AES 176	DR	SEQUENCE 1228 AA; 139665 MW; E86D9842341FB439 CRC64;
Db	106 QITENARNTALARQGLGSFRAYQOSLSDWLE -----NRDDARTSIVSLVTOYIALE 158	Qy	Query Match 31.5%; Score 1071.5; DB 2; Length 1228;
Query	177 HFRNSMSPS PAVKSPKVEVLFLPFTYQDAQVGEEMGYSSEDAEFPYHROLKL 236	Db	Best Local Similarity 36.6%; Prod. No. 3.e-61; Mismatches 248; Indels 59; Gaps 19;
Db	159 DFLNAMPLA PRKPHFLDQLG16BFHTRLQ 218	Qy	Matches 246; Conservative 119; Mismatches 248; Indels 59; Gaps 19;
Query	237 TQOYTDHCVNWNVNGLNGLRGSTDYDAWTKYKFRAREMTLTVLDLIVLSPFYD1RLYSKV 296	Db	1 MNPNRNRSEHDTRIKVTPNSLQTNTNQYPLADNPNSTLBEIINYKEFLRMTEDSSTEVIDNS 60
Db	219 TRDSDYC EWNTGLNSLRGTNAASWYNNQFRDLTLGVLDLVALPFSYDRTYPTINT 278	Qy	1 MTSRKNEENIINAVSNHSAQMD-----LLPARDIESLCLAEAGNN--IDPQ 45
Query	297 KTELTRDITDTP1-----FSNLNTQEQVGPFTLUSIS-NISRKRPHFLDQLG16BFHTRLQ 348	Db	61 TVKDAVGTCISVQGILGVGVPAGALTSPYQSFPLNTIWPSPADPKAFMAQVEVLIDK 120
Db	279 SAQLTREVVYDIA1GATGVNMASHWYNNMAPSFAIEA1AIRSPHLLDFEQLTIFS_AS 337	Qy	61 TVDAAWPNGKVYL--GTVKUDFQSQYDQK-NETSTQTYDTSKRNNGHVSAQDSIDQLP 461
Query	349 PGXFKGDSSP1VTRPSIGSSKTK1TSPPYG--DKSTTEPVQKLSFGOKVYRTAN 406	Db	46 VSASTVQGTQINIAGRILGVGVPAGQLAQSFSPYLGEMWPRGRDQWTFLEHVEQLINQ 105
Db	338 SRWNRTRHNTYWRGHTIQRPGIGLANT-----HGATWTSVNV-TURFASDVRYRTESY 393	Qy	121 KIEEYAKS KALAELQGLQNLQNFEDYVNAIWSKCKTPLSLRSKRSQDRIRE-LFSQL--AES 176
Query	407 TDVAAWPNNGKVYL--GTVKUDFQSQYDQK-NETSTQTYDTSKRNNGHVSAQDSIDQLP 461	Db	106 QITENARNTALARQGLGSFRAYQOSLSDWLE -----NRDDARTSIVSLVTOYIALE 158
Db	394 AGVLLW--GIVYLEPIHGPTVRFNTNEQNSDRTGANTNSQYESPGLQKDSETELP 450	Qy	177 HFRNSMSPS PAVKSPKVEVLFLPFTYQDAQVGEEMGYSSEDAEFPYHROLKL 236
Db	338 SRWNRTRHNTYWRGHTIQRPGIGLANT-----HGATWTSVNV-TURFASDVRYRTESY 393	Db	159 DFLNAMPLA PRKPHFLDQLG16BFHTRLQ 218
Query	462 ETIDDEPLEKAYSHQUNYAYACEFLM0D8RGT1PF7WTHRSVDFNTIDAKITOLPVVVKAY 521	Qy	237 TQOYTDHCVNWNVNGLNGLRGSTDYDAWTKYKFRAREMTLTVLDLIVLSPFYD1RLYSKV 296
Db	451 ETTERPNVSYSHRLSHIGIILQS -RNVPUVSWTHRSADRINTIGPNRITQIPMVKAS 508	Db	219 TRDSDYC EWNTGLNSLRGTNAASWYNNQFRDLTLGVLDLVALPFSYDRTYPTINT 278
Qy	522 ALSSGASITLGGPTGGTGNMFLKESSNSIAKFKVTLNSBALLYRVRIRYASTTNLRLP 581	Qy	297 KTELTRDITDTP1-----FSNLNTQEQVGPFTLUSIS-NISRKRPHFLDQLG16BFHTRLQ 348
Db	509 ELPGQSTTVRGPGPFGDIL-RRNTGGPPIRVTWNPQNSDRTGANTNSQYESPGLQKDSETELP 566	Qy	407 TDVAAWPNNGKVYL--GTVKUDFQSQYDQK-NETSTQTYDTSKRNNGHVSAQDSIDQLP 461
Qy	582 VQNSN--NDELFLVYINKTMKODDLTYQTFDLATTSNMGSGDKNELLIGAESFVSNE 638	Db	394 AGVLLW--GIVYLEPIHGPTVRFNTNEQNSDRTGANTNSQYESPGLQKDSETELP 450
Db	567 VSRGGTTVNNFRFL--RMMNSGDELKYCNGNEVRAFFTPTFTQIDIRTSIQLSGNG 623	Qy	462 ETIDDEPLEKAYSHQUNYAYACEFLM0D8RGT1PF7WTHRSVDFNTIDAKITOLPVVVKAY 521
Qy	639 KIYDKEIETIPV 650	Db	451 ETTERPNVSYSHRLSHIGIILQS -RNVPUVSWTHRSADRINTIGPNRITQIPMVKAS 508
Db	624 EVYIDKIEIETIPV 635	Qy	522 ALSSGASITLGGPTGGTGNMFLKESSNSIAKFKVTLNSBALLYRVRIRYASTTNLRLP 581
Q9NNM5	PRELIMINARY;	Db	509 ELPGQSTTVRGPFGDIL-RRNTGGPPIRVTWNPQNSDRTGANTNSQYESPGLQKDSETELP 566
AC	Q9NNM5;	Qy	567 VSRGGTTVNNFRFL--RMMNSGDELKYCNGNEVRAFFTPTFTQIDIRTSIQLSGNG 623
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	Db	639 KIYDKEIETIPV 650
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	Qy	

RESULT 27

Q9NNM5 PRELIMINARY;
 AC Q9NNM5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DR	Pfam; PF03944; Endotoxin_C; 1.	RL Submitted (JAN-2004) to the EMBL/GenBank/DBDJ databases.
DR	Pfam; PF00555; Endotoxin_M; 1.	DR EMBL; AY518201; AA R98783; 1;
DR	Pfam; PF03945; Endotoxin_N; 1.	DR GO; GO:0005102; P:receptor binding; IFA.
KW	Direct protein sequencing; Sporulation; Toxin.	DR GO; GO:0006932; P:defense response; IFA.
SEQUENC	1160 AA; 130425 MW; C16CDB912EEB8751 CRC64;	DR InterPro; IPR009079; 4-helix cytoxin.
Query Match	Score 1060; DB 1; Length 1160;	DR InterPro; IPR011178; Endotoxin.
Best Local Similarity	37.1%; Pred. No. 1.8e-60;	DR InterPro; IPR005639; endotoxin_C.
Matches 254; Conservative 116; Mismatches 254; Indels 60; Gaps 21;	DR InterPro; IPR005639; endotoxin_N.	
Qy	1 MNPNNRSEHDITIKTPNSSELTQNHQYPADNPNSTLEBNYKEPLRMEDSSTEVLDS 60	DR InterPro; IPR08919; Gal-bind_Like.
Db	1 MSPNNONEVIIIDALSPTSYSDNSTRYPLANDQNTNLQMMNYKDLYKMTESTNAELSRNP 60	DR Pfam; PF03944; Endotoxin_C; 1.
Qy	61 ---TVKDAVGTG1SUVGG1LGVYGVPPAGALTSFYOSFLNTIWP5-DADPKAFMAOYE 115	DR Pfam; PF00555; Endotoxin_M; 1.
Db	61 GTPISAQDAVGTGDIVSTTISGQIPVUGEVFSLGSIGLMPNSNNENWQ1FMNRP 120	DR Pfam; PF03945; Endotoxin_N; 1.
Qy	116 VLDKKEIEYAKSVALAEQGLQNNFEDVNALNSWKTPSLRSRSKRSQDRILEFSQAE 175	DR SEQUENCE 1160 AA; 130452 MW; C794F99AD1397188 CRC64;
Db	121 ELIDKILDSVRSRAIDANSRAVEYQNALDWRKNP---HSTRSALVAKERGNAE 177	Query Match 31.1%; Score 1060; DB 2; Length 1160;
Qy	176 SHFRNSMSPSPAVSKPSKEVLLPEPTYAQANTHLLKDAQVGEENGYSSSEDAEYHQLK 235	Best Local Similarity 37.1%; Pred. No. 1.8e-60;
Db	178 AILRTNMGGFSOTNQTYETPLPPTYQAASLHLYNVRDQVQYKGKWPQNDIDLYKEQVS 237	Matches 254; Conservative 116; Mismatches 254; Indels 60; Gaps 21;
Qy	236 LTQQYTDHCVNWNVNGLNGLQGSGTSDAWYKFNRFREMTLTVIDLVLFPFDYRLSKG 295	Qy 1 MNPNNRSEHDITIKTPNSSELTQNHQYPADNPNSTLEBNYKEPLRMEDSSTEVLDS 60
Db	238 YTARYSDHCTQWYNAGLNKURGTGAKQWVYDNRPRRNMMVLDLVALEPNYDARIYLPB 297	Db 1 MSPNNONEVIIIDALSPTSYSDNSTRYPLANDQNTNLQMMNYKDLYKMTESTNAELSRNP 60
Qy	296 VKTTELTRDIFTDP1FSLNTLQE-----YG-----PTFLSIEINSIRKPHLFDYLOGIEF 343	Qy 61 ---TVKDAVGTG1SUVGG1LGVYGVPPAGALTSFYOSFLNTIWP5-DADPKAFMAOYE 115
Db	298 TNAEATRETRDTPGSSYVYQGSSTLISWDMIPAALPSSTLNLRRPDEFTTLLQEIYRML 357	Db 61 GTPISAQDAVGTGDIVSTTISGQIPVUGEVFSLGSIGLMPNSNNENWQ1FMNRP 120
Qy	344 HTRL-QPGYFGKDSFNTWGSQNYVETRPSQGS-KTITSFYGDKSTPEVQKLSFDGQK-V 400	Qy 116 VLDKKEIEYAKSVALAEQGLQNNFEDVNALNSWKTPSLRSRSKRSQDRILEFSQAE 175
Db	358 YTSFRQNGTI---EYNNYNGQRLTTSYIYGSFNPKYSGVLAGADEIIIV-----GQNDI 409	Db 121 ELIDKILDSVRSRAIDANSRAVEYQNALDWRKNP---HSTRSALVAKERGNAE 177
Qy	401 YRTIANTDVAAPNGKVYUVTKVDFSQVDDQNETSTQTYDS-KRNGHVSAAQSDIDQ 459	Qy 176 SHFRNSMSPSPAVSKPSKEVLLPEPTYAQANTHLLKDAQVGEENGYSSSEDAEYHQLK 235
Db	410 YRVWW-TYIGRTYNS---LIGVNPNPTF---YSNNNTQKTYSKPKQFAGIKTIDSGBEL 461	Db 178 AILRTNMGGFSOTNQTYETPLPPTYQAASLHLYNVRDQVQYKGKWPQNDIDLYKEQVS 237
Qy	460 PPETTDEPPLKAYSHOLNAYAECFLMQMDRGT---IPFTTWTHRSVDFNTIDAEKITOL 515	Qy 236 LTQQYTDHCVNWNVNGLNGLQGSGTSDAWYKFNRFREMTLTVIDLVLFPFDYRLSKG 295
Db	462 TYEN----YQSTSHRVSTITSFEIKSTGSTVQGVPVIGWTSSASINNFYATKLSQI 516	Db 238 YTARYSDHCVQWNTAGLNKURGTGAKQWVYDNRPRRNMMVLDLVALEPNYDARIYLPB 297
Qy	516 PIVKAYALSSGA--SIIEGPGFTCGNLLFLKESSNSIAKFKVTLNSAALLQRYRVRIRYA 573	Qy 296 VKTTELTRDIFTDP1FSLNTLQE-----YG-----PTFLSIEINSIRKPHLFDYLOGIEF 343
Db	517 PINKASRTSGGAVWNFOEGL-YNGGPVNKLSGSSQVNLRYVATDAKGASQRYRVRIRYA 575	Db 298 TNAEATRETRDTPGSSYVYQGSSTLISWDMIPAALPSSTLNLRRPDEFTTLLQEIYRML 357
Qy	574 S-----TINLRLFQVNSNDFLVIYINNTMNDLITYQTQFDLATTNS-NNGFSGDKN 626	Qy 344 HTRL-QPGYFGKDSFNTWGSQNYVETRPSQGS-KTITSFYGDKSTPEVQKLSFDGQK-V 400
Db	576 SDRAGKFTSSRSPENPATYASASTAYTN-TMSTNASLTYSTFAYAESGPINLGSSSRT 634	Db 358 YTSFRQNGTI---EYNNYNGQRLTTSYIYGSFNPKYSGVLAGADEIIIV-----GQNDI 409
Qy	627 LIIGAEPSVNEKYYIDKIEFIPV 650	Qy 401 YRTIANTDVAAPNGKVYUVTKVDFSQVDDQNETSTQTYDS-KRNGHVSAAQSDIDQ 459
Db	635 FDISITKEAGAANLYIDREFIPV 658	Db 410 YRVWW-TYIGRTYNS---LIGVNPNPTF---YSNNNTQKTYSKPKQFAGIKTIDSGBEL 461
RESULT 30	PRELIMINARY;	Qy 516 PIVKAYALSSGA--SIIEGPGFTCGNLLFLKESSNSIAKFKVTLNSAALLQRYRVRIRYA 573
ID	Q6R2R6	Db 517 PINKASRTSGGAVWNFOEGL-YNGGPVNKLSGSSQVNLRYVATDAKGASQRYRVRIRYA 575
AC	Q6R2R6;	Qy 574 S-----TINLRLFQVNSNDFLVIYINNTMNDLITYQTQFDLATTNS-NNGFSGDKN 626
DT	05-JUL-2004 (TREMBrel. 27, Created)	Db 576 SDRAGKFTSSRSPENPATYASASTAYTN-TMSTNASLTYSTFAYAESGPINLGSSSRT 634
DT	05-JUL-2004 (TREMBrel. 27, Last sequence update)	Qy 627 LIIGAEPSVNEKYYIDKIEFIPV 650
DT	05-JUL-2004 (TREMBrel. 27, Last annotation update)	Db 635 FDISITKEAGAANLYIDREFIPV 658
OS	Bacillus thuringiensis	RESULT 31
NCBI TaxID	1428;	Q8KNY2
OX		ID Q8KNY2; PRELIMINARY;
RP		AC Q8KNY2; PRT; 1231 AA.
RA		DT 01-OCT-2002 (TREMBrel. 22, Created)

Qy	637 NEKIIYDKEIFIPV 650	Qy	629 NAEVIIIDREFEFIPV 642
Db	629 NAEVIIIDREFEFIPV 642	Db	629 NAEVIIIDREFEFIPV 642
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)	DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	CRYBII.	DE	CRYBII.
GN	Name=CRYBII;	GN	Name=CRYBII;
OS	Bacillus thuringiensis.	OS	Bacillus thuringiensis.
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID:1428;		NCBI_TaxID:1428;	
RN	[1]	RN	[1]
RA	SEQUENCE FROM N.A.	RA	SEQUENCE FROM N.A.
RA	Isakova I. A., Isakov Y. B., Rynnar' S. E., Yarovoi S. V.;	RA	Isakova I. A., Isakov Y. B., Rynnar' S. E., Yarovoi S. V.;
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.	RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AY18457; AAM3496.1; -.	DR	EMBL; AY18457; AAM3496.1; -.
DR	HSSP; P02656; 1CIV.	DR	HSSP; P02656; 1CIV.
DR	GO; GO:0005102; F: receptor binding; IEA.	DR	GO; GO:0005102; F: receptor binding; IEA.
DR	GO; GO:0009405; P: defense response; IEA.	DR	GO; GO:0009405; P: defense response; IEA.
DR	GO; GO:0009452; P: pathogenesis; IEA.	DR	GO; GO:0009452; P: pathogenesis; IEA.
DR	InterPro; IPR001178; Endotoxin.	DR	InterPro; IPR001178; Endotoxin.
DR	InterPro; IPR005639; endotoxin_N.	DR	InterPro; IPR005639; endotoxin_N.
DR	InterPro; IPR008979; Gal_bind_Like.	DR	InterPro; IPR008979; Gal_bind_Like.
PFam	PF00555; Endotoxin_M; 1.	PFam	PF00555; Endotoxin_M; 1.
PFam	PF03945; Endotoxin_N; 1.	PFam	PF03945; Endotoxin_N; 1.
SEQUENCE	1231 AA; 139764 MW; C9F284BA9297EA00 CRC64;	SEQUENCE	1231 AA; 139764 MW; C9F284BA9297EA00 CRC64;
Query Match	30.9%; Score 1053; DB 2; Length 1231;	Query Match	30.9%; Score 1053; DB 2; Length 1231;
Best Local Similarity	36.1%; Pred. No. 5.5e-60;	Best Local Similarity	36.1%; Pred. No. 5.5e-60;
Matches 243;	Conservative 114; Mismatches 261;	Matches 243;	Conservative 114; Mismatches 261;
Indels	56; Gaps 17;	Indels	56; Gaps 17;
Qy	1 MNPNTSEHDITKVTPNSEQCTINHNPQLADNPNSTLLELNKKEPLMTEDS---STEV 56	Qy	1 MNPNTSEHDITKVTPNSEQCTINHNPQLADNPNSTLLELNKKEPLMTEDS---STEV 56
Db	1 MTSNRKNEELI----NALSPTVSNPST---QMLNLPDARL-EDSLCVAEVNN 46	Db	1 MTSNRKNEELI----NALSPTVSNPST---QMLNLPDARL-EDSLCVAEVNN 46
Qy	57 LDNSTVDAVGIGISVVGQILGVGVPPAGALTFSYQOSPLNTIWPSPDAPWKAQAEV 116	Qy	57 LDNSTVDAVGIGISVVGQILGVGVPPAGALTFSYQOSPLNTIWPSPDAPWKAQAEV 116
Db	47 IDPFPVSASTVQCGINIGRQGQFVQGQFQGQFQGQFQGQFQGQFQGQFQGQFQ 106	Db	47 IDPFPVSASTVQCGINIGRQGQFVQGQFQGQFQGQFQGQFQGQFQGQFQGQFQ 106
Qy	117 LIDKKIREYAKSALAEQGLQGLONFQDYNALNSWIKPLSLRSKRSODRFLFQSOA 176	Qy	117 LIDKKIREYAKSALAEQGLQGLONFQDYNALNSWIKPLSLRSKRSODRFLFQSOA 176
Db	107 LIRQQVENTRNNTAIALEGLGRGRYRVSQQALETWLD--NNDARSRSIILERYAEL 163	Db	107 LIRQQVENTRNNTAIALEGLGRGRYRVSQQALETWLD--NNDARSRSIILERYAEL 163
Qy	177 HFRNSMPSFAVSKEFVLFLPVTQAAANTHLLIJKDAQVFGETWGYSSDVAEFYHROLKL 236	Qy	177 HFRNSMPSFAVSKEFVLFLPVTQAAANTHLLIJKDAQVFGETWGYSSDVAEFYHROLKL 236
Db	164 DTTAIPFLFRNNEEVPLMLVYQAANTHLLIJKDAQVFGETWGYSSDVAEFYHROLKL 223	Db	164 DTTAIPFLFRNNEEVPLMLVYQAANTHLLIJKDAQVFGETWGYSSDVAEFYHROLKL 223
Qy	237 TQOYDHCVNTWAVGLRQGTYDAWKENPFRREMTLTDLIVLFPYDTRLYSKGV 296	Qy	237 TQOYDHCVNTWAVGLRQGTYDAWKENPFRREMTLTDLIVLFPYDTRLYSKGV 296
Db	224 TFEYSNHCVQWNTGQMLGQTAESWRYNQPRDLTIGLVLFPSPYDTRYPINT 283	Db	224 TFEYSNHCVQWNTGQMLGQTAESWRYNQPRDLTIGLVLFPSPYDTRYPINT 283
Qy	297 KTELTRDIFTDPI-----FSLNTLQEQYGPFLTENSI-RKPHFEDYLOGIEFHTR 346	Qy	297 KTELTRDIFTDPI-----FSLNTLQEQYGPFLTENSI-RKPHFEDYLOGIEFHTR 346
Db	284 SAGLTREYTDGPGRTNAPSGFSTNWNNNAASFSAEAIRPRPHLDPBOLTYI- 342	Db	284 SAGLTREYTDGPGRTNAPSGFSTNWNNNAASFSAEAIRPRPHLDPBOLTYI- 342
Qy	347 LQPGYFGKSDENYWSQHGNVYETRPSIGSSKTTISPFYGDKSTKTFVQKLSFGOKVYRTIAN 406	Qy	347 LQPGYFGKSDENYWSQHGNVYETRPSIGSSKTTISPFYGDKSTKTFVQKLSFGOKVYRTIAN 406
Db	343 ASRRWSSTQHMMYWGIRLNFRIGGTNTSTOGLNTNTSINP-TLQFTSDRVYRTESN 401	Db	343 ASRRWSSTQHMMYWGIRLNFRIGGTNTSTOGLNTNTSINP-TLQFTSDRVYRTESN 401
Qy	407 TDVAAPNGKVKVQYKTVDFQYD---DQRN -ETSTQTYDSKRKNHGHSAQDSIDOL 459	Qy	407 TDVAAPNGKVKVQYKTVDFQYD---DQRN -ETSTQTYDSKRKNHGHSAQDSIDOL 459
Db	402 A-----GTLNLLEPTVQGPVDPDRENTPQTYGTYTQDFTLQYKTVDFQYD---DQRN -ETSTQTYDSKRKNHGHSAQDSIDOL 454	Db	402 A-----GTLNLLEPTVQGPVDPDRENTPQTYGTYTQDFTLQYKTVDFQYD---DQRN -ETSTQTYDSKRKNHGHSAQDSIDOL 454
Qy	460 PPTTDEPLEKAYSHQUNYAECFLMMDQDRGTTIPPTWTHRSVDFEFTDAEKITQLPVVK 519	Qy	460 PPTTDEPLEKAYSHQUNYAECFLMMDQDRGTTIPPTWTHRSVDFEFTDAEKITQLPVVK 519
Db	455 PPTTERNYESYSHRLSHIGLIGNTLRA--PVYSSWTHSARNTNTGPNRITQPAVK 512	Db	455 PPTTERNYESYSHRLSHIGLIGNTLRA--PVYSSWTHSARNTNTGPNRITQPAVK 512
Qy	520 AVALSSGASITIEPGFTGCGNLLFLKESNSIAK---FKVTLNAAALLORYVRIRYASIT 576	Qy	520 AVALSSGASITIEPGFTGCGNLLFLKESNSIAK---FKVTLNAAALLORYVRIRYASIT 576
Db	513 GRFLFG-SV1SGPFGTGGDVRUNRNNQNIQNRGQYIEPQFTSTSTRYVRVRYASIT 571	Db	513 GRFLFG-SV1SGPFGTGGDVRUNRNNQNIQNRGQYIEPQFTSTSTRYVRVRYASIT 571
Qy	577 NLRFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 636	Qy	577 NLRFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 636
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Db	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628
Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFSGDKNELLIGAESTVS 628	Qy	572 SIEFLVQNSNDLFLVIVYINKTMKQDDLTYQTFDLATLNSNMGFS

Db	121	ELIDQRISSEQVRNALDAALGHDHYNEVLAALBEWLERPNGARANLAQFR----FENLH 176	Qy	1	MNPNNRSEHDITKIVTPNSELQTNHNPYQPLADNPNSTL--ELNYKEFLRMTEDSSTEVL 57
Qy	176	SHFNRNSMPSE---AVSKKEVLFLIPTYQDAANTHLLKKDAQVFGEEWGSSEDAEPPYH 231	Db	1	MTSRRKNEEI-----WALSIPIAVSNHSAQMNUSTDARIEDSCTIAEGNN---I 47
Db	177	QLFVYSQMPFGSGPGERSERDAVALLTVYQAAANLHLLKKDAEYLGARNLQOINLYFN 236	Qy	58	DNSTVTKDAVGTGIVSGVQILQHNGVPPFAGALTSFYQSFINTINTPSADPKAFAQAEVEYL 117
Qy	232	RQLKLQQTQDTCYCNWYNGGLNGLRGSTDAWVKFNREREMTILTVLDPFYDIL 291	Db	48	DPEVVASTVQTGGINAAGRILGIVGVPFACQIAFSSFLVGEMLPRGRDWEIFLHVEQL 107
Db	237	AQDRTQITNNHCVATYNGLEUNLRTQNTESWNTYHQFRENTILMADIVLPYNNRQ 296	Qy	118	IDKKEEYAKSKALAELOCLOQNFDYNAALNSWKTPLSLRSKRSQDIRE-LFSQ--- 173
Qy	292	YSKGKVKTTELTRDIFDPIFLSLNTLQEQYG-----PTFLSTIENS-TKPHLFDFDQG 340	Db	108	IRQQVTTENTRTDALARQLGLNSFRAYQOSLEDWE-----NRDDARTRSVLYTQYIA 160
Db	297	YNGANPQLTREIYDTPVW-FNPNPANQGLCRRMWNNPYTFSELENTPRPHLFDRNLS 355	Qy	174	AESHFIRNSMPSFAVKFEEVLFLPTYAAQANTHLLKDAQVFGEMWGSSEDAEFYHQ 233
Qy	341	IEFHTRLQCGYFGKDSFNVWSGNVETRSIGSSKTIISPFYGDKSTEPVQKLSFDGKRY 400	Db	161	LELDFLNAMPLFAIRNQEYPLMVAQANLHLLRLDSLFSSEFGLTSQBTFRYERQ 220
Db	356	LTTINSHRF--ISSLNFMWDAGH-----TLLRSYNNNSA--VOEDSYGATTs 398	Qy	234	LKLTOQYTDHCVNMYVNGLNGLRGSTYDAWKVKNFREREMTILTVLDLIVLFPFYDILRYS 293
Qy	401	YRTANTDAAWPNGKVTIQLVTKYDFSQ-----NETSTOTYDSKRN 446	Db	221	VEKTREYSDCARWYNTGLUNLRGTNAEBSWLRYNQFRDLTGLVLDLVALFPSTDRYVp 280
Db	399	TRVTTINTG----NGTNNTIESTAVDFRSCLLGYGVHRAFSVFGGLFNGTI----SPAN 449	Qy	294	KGVKTELTTRDIFDPI-----FSUNLTLQYEGPTFUSIENS-TKPHLFDFQGKJEF 343
Qy	447	NGHVSQAQDIDQLP-PETTDEPLEKAYSHOLNAYAECFL--MQDRRGTT-----PFTWT 497	Db	281	MNTSAQLTREIYDPIGRNTNAPSGFASTNWNNNAPPSAIEAVIRPHLQDFPEQLTTI 340
Db	450	AGCRNLHDDRDELPLEENNGSP----SHRLSHV-TFLSFLTDQASGTRNSGAVPLVWA 503	Qy	344	HTRLQPGYFGKDSFNVWSGNVETRSTGSSKTIITSPFYGDKST--EPVQKLSEDGQKVY 401
Qy	498	HRSVDFEFTNTIDAKITOLFVYKAYALSSGASILIEPGFPFGGNLFLKESNSNASTAKFVTL 557	Db	341	FSVLS-RMSNTQYMNWYQHRLRSITRGLSST-----HGNTNTSINPV-TLQFTSRDVY 195
Db	504	RQDIDLNNTITANRITQFLVKASEIAACTTIVRGPGETGQDIL-RRTSAGTGTIVRN 562	Qy	402	RT-----IANTDVA-----WPN-----GKTY-LGVTKVDFQYDDQKNETST 438
Qy	558	NSAALLQQRVVRTRYASTTNLRLFVQNSNDFLVYININKTMKDDDTYQFDLATNSN 617	Db	396	RTESEAGINILLLTIPVNGVPWARENWRNPLNSLDRGSLLUYTGTGV-----GT 443
Db	563	NS-PLTQRTRVRFYASTDFENFFVIRGGTTVNNFTFPRTMNSGQESRYESTVTRFSTS 621	Qy	439	QTYDSKRNNGHYSAQDSIDQLPPTTDEPLEKAYSHQLNAYAECFLMDQRRGTIPFFWTH 498
Qy	618	MGFEGDKNEELIGAESFVSNEKITYIDKIEFIPV 650	Db	444	QLPDSE-----TELPETPTPNEYSHRLSNIR--LISGNTLRAPVYSWTH 489
Db	622	FNFLQIQDTLRLTVQFSSSQQVYDRIEIPV 654	Qy	499	RSYDFNTIDAKITQLPVKAVALSSASILIEPGFPFGGNLFLKESNSNIAKFKVTLN 558
Db	RESULT 36				
Q6PYW8		PRELIMINARY;	PRT;	849 AA.	
ID	Q6PYW8				
AC	Q6PYW8;				
DT	05-JUL-2004	(TREMBrel. 27, Created)			
DT	05-JUL-2004	(TREMBrel. 27, Last sequence update)			
DT	05-JUL-2004	(TREMBrel. 27, Last annotation update)			
DS	Cry1B type crystal protein (Fragment).				
OS	Bacillus thuringiensis (subsp. kurstaki).				
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.				
NCBI_TaxID	29339;				
RN	SEQUENCE FROM N.A.				
RP	SEQUENCE=1L;				
RC	CIBE-BACTU	STANDARD;	PRT;	1227 AA.	
RC	085805;				
AC					
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	05-JUL-2004	(Rel. 44, Last annotation update)			
DR	GO:0005102: F: receptor binding; IEA.				
DR	GO:0006552: P: pathogenesis; IEA.				
DR	GO:0009405: P: pathogenesis; IEA.				
DR	InterPro: IPR001178: Endotoxin.				
DR	InterPro: IPR005638: endotoxin_C.				
DR	InterPro: IPR005639: endotoxin_N.				
DR	Pfam: PF008919: Gal bind like.				
DR	Pfam: PF00555: Endotoxin_M.				
DR	Pfam: PF03945: Endotoxin_N.				
FT	SEQUENCE 849 AA;	95886 MW;	PCB98195787CF763	CRC64;	
SQ	Query Match 29.7%; Score 1013; DB 2; Length 849;				
Best Local Similarity 34.9%; Pred. No. 1.e-57;					
Matches 243; Conservative 123; Mismatches 226; Indels 104; Gaps 23;					
OX	NCBI_TaxID=1428;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=NRRL B-18672 / PS158C2;				
RC	"Bacillus thuringiensis" genes encoding lepidopteran-active toxin.				
RC	Payne J.M., Cummings D.A., Cannon R.J.C., Narva K.E., Stelman S.;				
RC	Strain=NRRL B-18672 / PS158C2;				
RC	"Bacillus thuringiensis" genes encoding lepidopteran-active toxin.				
RC	Patent number US7237378, 03-MAR-1998.				
CC	-1- FUNCTION: Promotes colloidal lysis by binding to the midgut				
CC	epithelial cells of many lepidopteran larvae.				
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during				

Qy	418 YLGYTIVDPSQYDDQKNEFSTQYD-----SKRNNNGIVSAQDSIDQUPPETDEPLEK 470	Matches 232; Conservative 124; Mismatches 258; Indexes 72; Gaps 17;
Db	416 Y-SWDTNFTYIPLLSSGQVSGISGYTQGIPAVCLQQRN-----STDEPSLNPEGDIFR 466	Qy 1 MNPNRSEHDTIKVTPNSELQTNHNOYPLADNPNSTLRLRNYKEFLRMTEDSSTEVLDNS 60
Db	-	Db 1 MNPNRNPNEYEIIDAPYCGPSDDVRYPIASDPAQAFQMNAYKEYLQTYDGTGSLNP 60
Qy	471 AYSHOLNAYECFLMDRR-----GTLPEFTWTHRSYDFEFTNTDAEKITOLPVPKAYA 522	61 TV---KDAVGTGTSISVVGQILGVYGVPPAGALTSFXYQSFNLNTIWP-SDADPWAFAKMAQE 115
Db	467 NYSHRLSHITQYRFOATQSGSPSTVSAHPTCWTWHDVLNTITANQITQDPLVKAYB 526	Db 61 NLSINPDRVQTLQGIVNIVRLGFVPPGAGLVFTYTFELNQWQPTNDNAWVEAFAQME 120
Qy	523 LSSGASITISPGFGTGNNLFLKESSNSTAKFKYTLNSAALLQYRVRYRAYERASTNLRFV 582	61.6 VLDKIKIEEYAKSKALAEQGLONNEDVYALNWSKTPLSRSKRSQDRIRELFSQAE 175
Db	527 LSSGATVPGPFGTGGDV--RRTNTGGFAIRSV-TGFLQTYRIRYRAYERASTIDFDFV 584	Db 121 ELIDQKISAAQVVRNALDDLTGLHDYEEYLAEEWLERPNGARA---NLVTOFRFENLH 176
Qy	583 QNSNNDFLIYIYINKTMNKDDLTQTFDIAATTNSNMGFSGDKNEELIGAESFSVNEKTYI 642	176 SHFRNSMPSFAV---SKPEVFLPLTYAQAANTHLLKDAOVFGEEMGYSSEDAEFPYH 231
Db	585 TRGGTTINNFRFTRTMNRQSRSRVEYRVEFTTPENFTQSQDIRTSIQLGSNGEYVL 644	Qy 177 TAFVTRMPSFGTGPQSQRDAVLLTVYAAQANHLKLKDAEYIYARGLQOCQINLYFN 236
Qy	643 D 643	Db 232 RQLKLTQYTDHCVNWNNGLNGLRGSTYDANVTKFNRFRREMTLTDLIVLFPFYDTRL 291
Db	645 D 645	Db 237 AQOFRTRAYTNHCEVTEYRGLEDYRGTNTYRFRERMLAMOLVALPFYNYRQ 296
RESULT 39		
C9A_BACTA	STANDARD;	Qy 292 YSGKVKPLBLRDLTDP1FSLNTLQXGP-----TFLUSIENS-IRKPHL 334
AC	C92N19; BACTA	Db 297 YPNGANPQITRELYTDPIV-----YNPANGICRWRGWNNPYNTFSELENAFIRPHL 349
DT	16-OCT-2001 (Rel. 40, Created)	Qy 335 FDYLQGIBFHTRIQLQGYFGKDSFNYWSGNVYETRPSIGSSKTITSFYGDKSTEPVQLLS 394
DT	16-OCT-2001 (Rel. 40, Last sequence update)	Db 350 FERLNRLTISRNRYTAPPTNSFLDWSHTLQSQHA--NNPPTYETSYQGITSNTRLPNT 407
DE	05-JUL-2004 (Rel. 44, Last annotation update)	Qy 395 FDGOKVYRTIANTDVAAMPNGKTYVDFQYDOKNETSTQYDTSKRNNNGHVSQD 454
DE	Pesticidal crystal protein cry9ca (Insecticidal delta-endotoxin CryIXE(a)) (Crystalline entomocidal protoxin) (130 kDa crystal protein)	Db 408 TNGARA-----IDSRAFNFGNLYANLYGV-----SSLNINFTGMSBEITNAANTCQD 455
GN	Name=cry9Ea; Synonyms=cryIXE(a);	Qy 455 SIDQLPPTTDE_PLEKAYSHOLNAYAECFLMDRR-----GTPFPTWTHRSVDFNT 506
OS	Bacteria: Firmicutes; Bacillales; Bacilliaceae; Bacillus.	Db 456 L-----TTTEELPLENNFNFLSHVFLRFLNTTOGGPLATGFVPTVWTRBDDFTNT 509
OX	NCBI_TaxID=1433;	Qy 507 IDABKITOLPVVKAIALSGAS1IEPGFTGGNLLFLKEXSSNIAKFVTLNSAALLORY 566
RN		Db 510 ITADRTTOLPVWKAISELGGTTVKGPFQFTGGDIL--RRTDGAVGTVANVN-APLTOQY 567
RP	SEQUENCE FROM N.A.	Qy 567 RYRIRYASTTN--LRLFVQNSNNDFLVYIYKTMNKDDLTQYTFDATTNSMNGFSGDK 624
RA	Midoh N., Oyama K.;	Db 568 RYRIRYASTTSFVNFWNNSSAFT--LPSMAGQNSLTSFNTLBEVTFIRFSQSD 624
RA	"Bacillus thuringiensis cry gene for insecticidal crystal protein.";	Qy 625 NEIJIGAESFSVNEKUYIDKIEPIV 650
RL	Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.	Db 625 TTURLNIFPSISQEVVYDQLSTVPI 650
CC	-!- FUNCTION: Promotes colicidomotic lysis by binding to the midgut epithelial cells of insects.	
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.	
This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
EMBL; AB011496; BAA34908.1;	RESULT 40	
InterPro; P07130; IDUC;	Q71RP4	RN PRELIMINARY; PRT; 1150 AA.
InterPro; IPR001178; Endotoxin_C;	AC Q71RP4;	OS Bacteriia; Firmicutes; Bacillales; Bacillaceae; Bacillus.
InterPro; IPR005638; endotoxin_N;	DT 05-JUL-2004 (TREMBLref. 27, Created)	GN Name=cry9Ea;
DR	DR Li C., Zhang J., Li G., Huang D.;	RN SEQUENCE FROM N.A.
DR	DR Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	RC STRAIN=B-Hm-16;
DR	DR EMBL; AF358863; AAO12908.1;	RA Li C., Zhang J., Li G., Huang D.;
DR	DR GO; GO:0005102; P:receptor binding; IEA.	RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR	DR GO; GO:0008952; P:defense response; IEA.	DR GO; GO:0009405; P:pathogenesis; IEA.
DR	DR GO; GO:0009405; P:defense response; IEA.	DR InterPro; IPR01178; Endotoxin.
SEQUENCE 1150 AA;	129895 MW;	SQ 7D6AB93D6EDC97EB CRC64;
Query Match 29.2%; Score 995; DB 1; Length 1150;	Best Local Similarity 33.8%; Pred. No. 3.le-56;	

DR	InterPro; IPR005638; endotoxin C.	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
DR	InterPro; IPR005639; endotoxin N.	
DR	InterPro; IPR008979; Gal_bind_Like.	
PFam	PF003944; Endotoxin C; 1.	
DR	PFam; PF000555; Endotoxin M; 1.	[1] _SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
DR	PFam; PF003945; Endotoxin N; 1.	STRAIN=VRCP B-1166;
DR	SEQUENCE 1150 AA; 129895 MW; 7D6AB93D6EDC97EB CRC64;	MEDLINE=99330166; PubMed=10403372; DOI=10.1016/S0014-5793(99)00650-X;
SQ		RA Wojciechowska J.A.; Lewitin E.; Revina L.P.; Zalunin I.A.,
		RA Chestukhina G.G.;
		"Two novel delta-endotoxin gene families cry26 and cry28 from Bacillus thuringiensis sp. <i>Finimus</i> .";
		RL FEBS Lett. 453:46-48 (1999).
Qy	1 MNPNNSREHDTIKTVPNSELQINHNOYPLADNPNSTLEENYKEFRMTDSSTEVLQNS 60	CC -!- FUNCTION: Promotes colloidiosmotic lysis by binding to the midgut epithelial cells of insects.
Db	1 MNPNNSREHDTIKTVPNSELQINHNOYPLADNPNSTLEENYKEFRMTDSSTEVLQNS 60	CC -!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.
Qy	61 TV---KDAVGTGSIYVGQTLGVGVGYPPGAGALTSPYQOSFNTLWPSDADPKMAQVE 115	CC -!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.
Db	61 NISINSPRDVLQDQINVGQTFVQGQFLGVGPAGQLWPTFLNQLWPNDNAWEAMQAE 120	CC -!- SIMILARITY: Belongs to the delta endotoxin family.
Qy	116 VLDKKEBEYAKSKAELQQLQNNEDYDNLNSMKTKTISLRSKRSQPIRELFSQE 175	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license at http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch.
Db	117 DLDQKLISAVVRNALDDLTGLHDYEEYLAEEELERNGARA---NLVTOFENLH 176	CC
Qy	176 SHFRNSMSPFAV---SKFBDLFLPYAQAAANTHLLKDAQVFGEWGKSSVEDAEPFH 231	CC
Db	177 TAVTVMPSFTGPGSORDAVIALITYQAQANHLLKDAEYCARWGLQGQONLYFN 236	CC
Qy	232 ROLKLTQYTTDHCVNYYNVGLNGLRGSSTYDAWVKENFRFRENTLTVDLIVLFPFDIIL 291	CC
Db	237 AQERTPRYYINHCVETNVRGLEDVRGNTNLSMLNTHFRFRENTLWAMDLVLFPPFNVRQ 296	DR EMBL; APF12897; AAD25075; 1; -.
Qy	292 YSKGVVTEFLTDLFTDPLFESLNTLQEQYGP-----TFLSLENS-TRKPHU 334	DR HSSP; P07130; 1, DLC.
Db	297 YPNGANFQLTRIYTDIV-----YNPANQGICRRGNGNPNTSELENAFTRPHL 349	DR InterPro; IPR001178; Endotoxin.
Qy	335 FDYLOGTEFHTRLQPGYFGKDSFNTMSGNTVETRPSIGSKTTITSPYFGKSTEWPQKLS 394	DR InterPro; IPR005639; endotoxin_N.
Db	350 FERLNLITISRNRYTAPTTNSFLDVSQHQSQA---NNPPTTYETSYQQTTSNTRLENT 407	DR InterPro; IPR008979; Gal_bind_Like.
Qy	395 FDGQKYYRTIANTDVAWPGKRYGTVKTDQYDQKNTSTQYDSDRNGHVAQD 454	DR Pfam; PF03944; Endotoxin_C; 1.
Db	408 TNGARA----IDSRAFNFGNLYANLYGV-----SSLNIFPTGMSEITNAANTCQD 455	DR Pfam; PF03955; Endotoxin_M; 1.
Qy	455 SIDQLPPTDE-PLKEXASHOLNAYAECMMDQR-----GTPPFETWHSYDFFNT 506	DR Pfam; PF03945; Endotoxin_N; 1.
Db	456 L-----TTTEELPLLENNFNFLSHYTFLRLNNTTQGPLATLGFVTVWTRDVFNT 509	DR Direct protein sequencing; Sporulation; Toxin.
Qy	507 IDAEKITQLPVVKAYALSSGASIIIEGPGFTGGNLLFKKESSNSIAFKVTKTNSAALLQY 566	DR SEQUENCE 1163 AA; 131284 MW; 7B5DDEB51341908 CRC64;
Db	510 ITADRTQLPWVKAESGGTGVKGGTGGDIL-RRTDGAVGTRAYNN-APPTQOY 567	DR
Qy	567 RYRYYASTN--LRLPVONSNDFLVYIINKTMNKDDLYQTDFIATNTSMGFSGDK 624	DR
Db	568 RYRYYASTSFTPVNLFVNNNSAAGFT--LPSMTAONGSLTYESENTEVHTIREQSD 624	DR
Qy	625 NELIGAESPVSNEKYIYDKEBTFPV 650	DR
Db	625 TTRLN1PPS1SQQEVVTDKUBIVP1 650	DR
		Qy 232 RQLKLTQYTDHCVNYYNVGLNGLRGSSTYDAWVKENFRFRENTLTVDLIVLFPFDIIL 291
		Db 232 RLLRHSAEYDHCVNYYNTGKQLENSDAKSWFQINFRFRENTLSLVDVLFPAVDVKM 291
RESULT 41		Db 292 YSKGVVTEFLTDPLFPI-----PSLNTLQEYGPFLSIEINS-1RKPHLFYDLO 339
COAA_BACTF	STANDARD;	Db 292 YP1PTNQFLTREVYVIGKIGRNDSDHWSAN----AFPSNLSTLRTPHVVDYIK 346
AC	Q9X597;	Qy 16-OCT-2001 (Rel. 40, Created)
DT	16-OCT-2001 (Rel. 40, Last sequence update)	Db 05-JUL-2004 (Rel. 44, Last annotation update)
DT		DE Pesticidal crystal protein cry26Aa (Insecticidal delta-endotoxin
DE	CRYXXVIA(a) (Crystalline entomocidal protein cry26Aa (131 kDa crystal	DE Name=cry26Aa; Synonyms=cry26Aa, cryXXVIA(a);
GN		DE protein
OS		OS Bacillus thuringiensis (subsp. <i>finimus</i>).
		Qy 398 QKVRYRANTDVAWNG-----KVLYGTVKDFQSYYDDONNETSTQTYDSKR-- 445

Db	402	KNIYKII-----GSUPLQGPBPYQIGXVTPYFITRAVNFTVSSSK--TSVEKYSSKKR	453	Db	139	RA---NLYLQRFBLHALFVSSNIPSFGSPGSQRFQAGILVYAAQAANTHLLLADAEK	194
Qy	446	-NNGHVSAQD--SIDQLPBPETTDEPLEKAYSHQNLNYAACFLMDRR--GTPPFITWTH	498	Qy	215	FGEEWGYSSBBDVAFPHQKLK-TQOYTDHCVWVYNGLRSSTYDAWKENRFRREM	273
Db	454	YYSEGLPPEEQVFSTEQLPNNPSIAAPEHAYSHRLCHVTFTSVNGNKYSKDKLPLEFSWTH	513	Db	195	YGAWRGLRSEQQIGNYVFNELQTRTRDTHCVAAYNNGLAGLRTGTSAESWLKYHCFRREA	254
Qy	499	RSVDFENTIAEKITQLPVVKAYALSGASILLEGFTGNLFLKESSENSIAFKVTLN	558	Qy	274	TLTVDLTLVLPFDYIRLYSKGVTKTELTRDIFTDP-----IFSINTLQEYGP	320
Db	514	SSVDFDNYVPTKTLQPLATKGY---NYSIVKEPGFIGDDI--GKNGNQILGKYKVNV	567	Db	255	TLMAMDLILAFPLPFYNTTRVPIANPQLREVYDLPGLGPSEESSLFPEDRCLRVQETSAM	314
Qy	559	SAALLQRYRYRIRYASTNHLFVYONSNNDFLVYINKTMNKDDDLTYCOTFLATTSNM	618	Qy	321	TEFLSIENS-IRKPHLFDFYLOGIEBFHTRLQPGYFGKDSFNYWSGNVYETRPSIGSSKTITS	379
Db	568	DVS--QKYRPRVRIATETEGELGKIDGTVNLQYKTKAPGDPFLYKAFDYLSTFSTV	625	Db	315	TFSNIDENATISSPLFDTINNLMTYGSFSVHLTNQLEGWIGHSVTSSLASGPTTVLR	374
Qy	619	GFSGDKNELLITIGAEFFVSNB---KIVYDKEFIPVQ	651	Qy	380	PFYGDKS1STEPVQKLSPFGQKVR--TIAINTDVAAPNGKVLGTVKDVQDDQKNETS	437
Db	626	KFNNASSTI---ELFLQNRKTSQTGFLYLAGIEIIIPVK	657	Db	375	RNYG-STTSIVNYESFENDRDVYQINTRSHTLG-GFQNAPLF-GITRAQF-----YP	422
Qy	627	RESULT 42		Qy	438	TQYDSDKRNNGHVAQ--DSIDQLPETTDEPLEKAYSHQNLNAYCFL-----MDQR	487
Db	Q45745	PRELIMINARY;	PRT;	Db	423	GFTYSVTQRNALTCEQNYNSIDEPLSDBNEPISRSYSHRLSHITSYLRHVLTDGINY	482
ID	Q45745;			Qy	488	RGTIPFFWTHRSYDFNTTDAEKITOLPVKAYALSGASILLEGFTGNLFLKKESS	547
AC	Q45745;			Db	483	SGNLPITYWTHRDVDTLNTITADRTQLPLVSKFIPAGTTVRGPFGTGDDIL-RRTCV	541
DT	01-NOV-1996	(TREMBUREL. 01, Created)		Qy	549	NSTIAKEKVTLNNSAALQYRVRIRYASTNLRFLVQNSNNDFLYIYINKTMNKDDDLTQ	607
DT	01-NOV-1996	(TREMBUREL. 01, Last annotation update)		Db	542	GTRGTIRV-TTAPLATORYRIRFRASTNLFIGRDNQYXFDFERTMNGDRELVE	600
DE	01-NAR-2004	(TREMBUREL. 26, Last annotation update)		Qy	608	TFDLATMNSNMGSGDNELIIGAESFSNEK1YIDKLFIPV	650
DE	Delta-endotoxin (fragment).			Db	601	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
GN	Name=cryTX	gene;		Qy	609	TFDLATMNSNMGSGDNELIIGAESFSNEK1YIDKLFIPV	643
OS	Bacillus thuringiensis.			Db	610	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
OS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.			Qy	611	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
NCBI_TaxID	1428;			Db	612	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RN				Qy	613	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RP	SEQUENCE FROM N.A.			Db	614	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RA	Shevelev A.B., Svirinsky M.A., Karasin A.I., Kogan Y.N.,			Qy	615	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RA	Chestukhina G.G., Stepanov V.M.;	"Primary structure of the cryX*-the novel Delta-endotoxin-related gene from Bacillus thuringiensis" spp. <i>Galleriae</i> ;"		Db	616	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	617	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	618	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	619	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	620	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	621	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	622	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	623	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	624	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	625	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	626	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	627	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	628	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	629	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	630	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	631	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	632	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	633	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	634	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	635	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	636	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	637	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	638	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	639	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	640	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	641	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	642	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	643	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	644	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	645	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	646	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	647	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	648	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	649	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	650	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	651	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	652	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	653	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	654	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	655	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	656	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	657	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	658	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	659	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	660	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	661	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	662	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	663	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	664	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	665	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	666	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	667	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	668	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	669	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	670	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	671	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	672	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	673	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	674	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	675	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	676	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	677	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	678	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	679	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	680	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	681	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	682	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	683	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	684	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	685	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	686	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	687	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	688	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	689	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	690	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	691	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	692	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	693	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	694	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	695	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	696	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	697	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	698	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	699	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	700	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	701	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	702	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	703	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	704	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	705	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	706	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	707	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	708	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	709	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	710	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	711	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	712	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	713	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	714	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	715	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	716	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	717	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	718	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	719	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	720	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	721	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	722	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Qy	723	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643
RT	RT			Db	724	SPATREFTTDNFNFRQPOELISVFANAFSAGQEVYFDRIEIIPV	643

RT	airawai 7.29.";	255	LRGSTYDAWKENPRFREMTLTVDLILVLFFPYDIRLYSKGVKTELTDIFTDPIFSSLN-
RT	Mol. Microbiol. 3:229-238(1989).	260	2.17 LPSTYQDWITHNRLRDLTIVDIAAFFPYDNRRYPIQPGQLTREYTDPLINFNP 276
RN	SEQUENCE OF 1-756 FROM N.A.	314	TLOEYG--PTFLSIEENS IRKPHLFDYLOGIBFHTRIQPQGKFQDKDSTNYNSNYVETPRPS 370
RP	SPECIES=B.t.aizawai; STRAIN=7-29 / K26-21;	277	QLOSVAQPTFVNMESSAIRNPHFLDNLNLIFT---DWTSVGRNFYWGHRVIS-S 330
RC	Strizhov N;	371	IGSSKTTSPFYG-DKSTEPVQKLSEFGQKCYRTANTDVF---AAMPNGKVYL-GYTKV 424
PA	Strizhov N;	331	LIGGGNTSPFYG-REANGEPFRSFTFG- PVERTLSPTRLQQPQAPPNLRGEGV 389
RL	FUNCTION: Promotes colloidiosmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae including spodoptera species.	425	DFSYQYDQKNETSTQTYDPSKRNHGHQSDFDOLPPTTDEPLEKAYSHOLNYAECFLM 484
CC	-!- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	390	EFS---TPINSPFY---RGSGTV---DSLELPDDNSPREGYSHRUCHA--TF 434
CC	-!- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	485	QDRRGTTIPF----FTWTHRSYDFNTIDAEKITOLPVKVALSSASILEGPFGTGG 538
CC	-!- SIMILARITY: Belongs to the delta endotoxin family.	435	VQRSGT-PPLTGUVFWSWTHRSATLNTIDPERINQ1PLVKGFRVWGTSTVITPGFGTGG 493
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	539	NLLIUKESSNSIAKFKTILNSAALQRYRVRAYASTTNRLFV-----QSNN 587
CC	-----	494	DIL-RRTNTFGDFVQLQNNNS-PITQRQLRFYIASSRNDARVLTGAATSTGYGQSVN 551
CC	-----	588	DFLVITYINKTMKDDDLTQEDLATNSNMGFS-----GDKNELLIGAESPVSNKLY 641
CC	-----	552	---MPLQTCMEGENLTERTFRDFSNPFSRANPDIGISQPLFGAGS-ISSEGYX 606
EMBL	X07518; CAA30396.1; -.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
EMBL	M73251; AAQ22343.1; -.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
EMBL	X133620; CAA31951.1; -.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
EMBL	X96682; CAA85457.1; -.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
PIR	SO0944; S00944; S00944.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
PIR	SO04181; S04181.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
HSSPC	P02965; 1C1Y.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
DR	InterPro; IPR001178; Endotoxin.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
DR	InterPro; IPR005638; endotoxin C.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
DR	InterPro; IPR005639; endotoxin_N.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
DR	InterPro; IPR008919; Gal_bind_Type.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
PFAM	PRO3944; Endotoxin_C.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
PFAM	PF00555; Endotoxin_M.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
DR	PFAM; PRO3945; Endotoxin_N.	Db	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
KW	Sporulation; Toxin.	RESULT 44	Q6YNB8; PRELIMINARY; PRT; 1189 AA.
FT	CONFLICT 124 A -> E (In Ref. 1).	Q6YNB8	PRELIMINARY; PRT; 1189 AA.
FT	CONFLICT 294 A -> R (In Ref. 1).	ID	06YNB8; PRELIMINARY; PRT; 1189 AA.
FT	CONFLICT 366 N -> I (In Ref. 3).	AC	06YNB8; PRELIMINARY; PRT; 1189 AA.
FT	CONFLICT 376 380 WPPAPP -> CORRH (In Ref. 3).	DT	05-JUL-2004 (TREMBREL. 27, Created)
FT	CONFLICT 386 386 V -> G (In Ref. 3).	DT	05-JUL-2004 (TREMBREL. 27, Last sequence update)
FT	CONFLICT 405 405 T -> Q (In Ref. 1).	DT	05-JUL-2004 (TREMBREL. 27, Last annotation update)
FT	CONFLICT 453 453 H -> D (In Ref. 1).	DB	Delta-endotoxin (Insecticidal protein CryICa).
FT	CONFLICT 775 775 R -> A (In Ref. 3).	GN	Name=cryIC; Synonyms=cryICa;
FT	CONFLICT 853 853 V -> L (In Ref. 2).	OS	Bacillus thuringiensis.
FT	CONFLICT 864 864 G -> N (In Ref. 2).	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
FT	CONFLICT 931 931 D -> N (In Ref. 2).	OX	NCBI_TaxID=1428; NCBI_TaxID=1428;
SQ	SEQUENCE 1189 AA; 134715 MW; 36278685916AODP CRC64;	RN	[1] [2]
RN	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RN	Kao S.-S.; Hsieh F.-C.;	RA	SEQUENCE FROM N.A.
RN	Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.	RA	SEQUENCE FROM N.A.
RN	[3]	RA	SEQUENCE FROM N.A.
RN	STRAIN=c002;	RC	SEQUENCE FROM N.A.
RN	Chen Z., Wu X., Zhang J., Yao J., Huang D.;	RA	SEQUENCE FROM N.A.
RN	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	RL	SEQUENCE FROM N.A.
DR	42	DR	SEQUENCE FROM N.A.
DR	43 QFLVSNFPGGFLVGLIDFWG1VGPSSQ--WDAFLVQIEQLINERAFAPNAAATNL 99	DR	SEQUENCE FROM N.A.
DR	75 QILGVGVPPAGALTSFYSPNPLNTWPSADPKAFMAQEVILDKKIEYAKSKALAEI 134	DR	SEQUENCE FROM N.A.
DR	43 QFLVSNFPGGFLVGLIDFWG1VGPSSQ--WDAFLVQIEQLINERAFAPNAAATNL 99	DR	SEQUENCE FROM N.A.
DR	75 QILGVGVPPAGALTSFYSPNPLNTWPSADPKAFMAQEVILDKKIEYAKSKALAEI 134	DR	SEQUENCE FROM N.A.
DR	43 QFLVSNFPGGFLVGLIDFWG1VGPSSQ--WDAFLVQIEQLINERAFAPNAAATNL 99	DR	SEQUENCE FROM N.A.
DR	135 QGLQNNFEDYDYNALNSWKTPSLRSKRSQDRIBELFSAEHSERNMSMPSFAVSKFEVLF 194	DR	SEQUENCE FROM N.A.
DR	100 EGLGNNFNTIVTEAFKEWEDP--NNPAPTRTRVDRFRFLDGLLERDPSFRISGFEVPL 156	DR	SEQUENCE FROM N.A.
DR	195 LPTYQQAANTHLLIJKDAQFGEENYSSDVAFYHQLKLTCQYDCHCVMVNYVNGL 254	DR	SEQUENCE FROM N.A.
DR	157 LSVTAQANTHLLAIRLDSVIFGERMGLTINVNENYNRIRHIDEADICANTYNRGLIN 216	DR	SEQUENCE FROM N.A.

SQ	SEQUENCE	1189 AA;	134714 MW;	36276B685916A0DF CRC64;	DR	HSSP; P02965; 1CIV.
	Query Match	27.4%;	Score 934.5;	DB 2;	Length 1189;	GO:0005102; F; receptor binding; IBA.
	Best Local Similarity	36.3%;	Pred. No. 3e-52;	Length 1189;	GO:0006952; P; defense response; IBA.	
	Matches	242;	Mismatches 103;	Indels 95;	Gaps 27;	GO:0009405; P; pathogenesis; IBA.
Qy	21	QTNHINQ--YPLADNPNSTLSELNYKEFLRTEDSSTEVLND--STVDAVGTGISYVG 74	DR	InterPro; IPR011178; Endotoxin.		
Db	3	ENNONQCIPICNCLSPREEVLL--LGDGERISTGNSSTDISLSD- 42	DR	InterPro; IPR056318; endotoxin_C.		
Db	4	QFLGVVPPAGALTSPYSPFLNTIWPADPWAFAKMAVEFLIDVKKEBYAKSKALLE- 134	DR	InterPro; IPR056339; endotoxin_N.		
Db	43	QFLVSNFVPGGGFLVGLIDFWVGIVGPSQ--WDAFLVQIEQLINERIAEFAVAAIAN 99	DR	InterPro; IPR08919; Gal bind like.		
Qy	135	QGLQNNFEDVYNAWSKCTPLSLRKSDRTRFLSFQAEHSFRNSMSPFAVSKFEVLF 194	DR	Pfam; PF03944; Endotoxin_C_1.		
Db	100	EGLGNFNFTVTEAKPEWEQD--NNPAPTRTRVDRFLGLBLRDFESFRISGFEVLF 156	DR	Pfam; PF05555; Endotoxin_M_1.		
Qy	195	LPTYQAQANTHLLIJKDAQFGEENGYSSEDAFAYHQLQLTQCYTDHCVWVWVNGLNG 254	DR	Pfam; PF03945; Endotoxin_N_1.		
Db	157	LSVYQAQANHLLAIRDSTIGERGLTIVNENYNRJRHDEADANCANTYNRGINN 216	DR	SEQUENCE 1189 AA; 134684 MW; 9.8F8C1D978DF9451 CRC64;		
Qy	255	LRGSTYDAWVKNFRPRTMTLTVLIVTPFYDIRLYSKGVKTBLTDIRDTPFISLN- 313	DR	Query Match 27.4%; Score 932.5; DB 2; Length 1189;		
Db	217	LPKSTYQDNTYNNURRDLTTLVLDIAAFTPPNYNDRYIOPQVCPQLTREVYTDLINPNT 276	DR	Best Local Similarity 36.5%; Pred. No. 4e-52; Gaps 27;		
Qy	314	TLOEYG--IPTFLSIEIS-IRKPLFLSIEIS-IRKPLFLDYLQGIEFHTRLQPGYFGKDSFNYWSGNYVETRPS 370	DR	Matches 244; Conservative 101; Mismatches 226; Indels 97; Gaps 3 ENNONQCIPICNCLSPREEVLL--LGDGERISTGNSSTDISLSD- 42		
Db	277	QLQSYAQLPPFNMMESSAARNPHEDILNMLNLTIP---DWFSYGRNFVPGGHRVIS--S 330	DR	QY 21 QTNNHQ---YPLADNPNSTLSELNYKEFLRTEDSSTEVLND--STVDAVGTGISYVG 74		
Qy	371	IGSSTKTTSPFYG--DKSTEPVQKLSFDGQKVYRTANTD---AAWPNGKVKL-GVTKY 424	DR	Db 3 ENNONQCIPICNCLSPREEVLL--LGDGERISTGNSSTDISLSD- 42		
Db	331	LIGGENITISIYGRBANQEPSPRFIFNG--PVFRTLISNPTRLQLQWPAPPFLNLRGEGV 389	DR	QY 75 QILGVVGPFFAGALTSPYQFLNTIWPADPWAFAKMAVEFLDVKKEBYAKSKALLE 134		
Qy	425	DFSQYDDQKNETSTOTYDSKRNNGHVSADPSIDOLPPETDDEPLEKAYSHQLNAYABCPLM 484	DR	Db 43 QLQSVAQIQLPTENMMESSAIRNPHFLDILNNLIFT--DWPSVGRNEYWGGRHRVIS--S 330		
Db	390	EFS-----TPTNSFTY--RGRFTV--DSLTLPPLPENNSVPREGFSRHLCHA--TF 434	DR	Db 217 LPKSTYQDNTYNNURRDLTTLVLDIAAFTPPNYNDRYIOPQVCPQLTREVYTDLINPNT 276		
Qy	485	QDRRRTIPF-----FTWTHRSVDFNTIDAEKITQTLPVKAYALSSGASITEGPGFTG 538	DR	QY 314 TLOEYG--IPTFLSIEIS-IRKPLFLSIEIS-IRKPLFLDYLQGIEFHTRLQPGYFGKDSFNYWSGNYVETRPS 370		
Db	435	VQRSGT--PLLTGUVFSWTHRSATLNTDPERINQIPYKGRVWGGTSVIRGPGFITG 493	DR	Db 277 QLQSVAQIQLPTENMMESSAIRNPHFLDILNNLIFT--DWPSVGRNEYWGGRHRVIS--S 330		
Qy	539	NLLPLKKESSNSIAKFKVTHLNSAALQYRVRVYRFASTTMURLFY-----QNSNN 587	DR	QY 371 IGSSKTTSPFYG--DKSTEPVQKLSFDGQKVYRTANTD---AAWPNGKVKL-GVTKY 424		
Db	494	DIL--RRNTFSDFVSLQVNNS--PITQRYVLRFASSRDRVVLGAASITGVGGQVSN 551	DR	Db 331 LIGGENITISIYGRBANQEPSPRFIFNG--PVFRTLISNPTRLQLQWPAPPFLNLRGEGV 389		
Qy	588	DFLVYINCKTMNKKODDLTYQTDFLATTSNMGFS----GDKNELLITGAESFVSNKLY 641	DR	QY 485 QDRRRTIPF-----FTWTHRSVDFNTIDAEKITQTLPVKAYALSSGASITEGPGFTG 538		
Db	552	----MPLQKTMIEGENLTSRTPTRYTDSNIPSPRANPDDIGISEQPLTGAGS-ISSGRLY 606	DR	Db 425 DESQYDQKNETSTOTYDSKRNNGHVSQDSIDOLPPETTDEPLEKAYSHQLNAYABCPLM 484		
Qy	642	IDKIEFI 648	DR	Db 435 VQSGT--PLLTGUVFSWTHRSATLNTDPERINQIPYKGRVWGGTSVIRGPGFITG 493		
Db	607	IDKIEFI 613	DR	Db 390 EFS-----TPTNSFTY--RGRFTV--DSLTLPPLPENNSVPREGFSRHLCHA--TF 434		
Q9J877	RESULT 45	PRELIMINARY;	DR	QY 539 NLLPLKKESSNSIAKFKVTHLNSAALQYRVRVYRFASTTMURLFY-----QNSNN 587		
AC	09J877;	PRT; 1189 AA.	DR	Db 494 DIL--RRNTFSDFVSLQVNNS--PITQRYVLRFASSRDRVVLGAASITGVGGQVSN 551		
DT	01-OCT-2000 (TREMBLrel. 15, Created)		QY 588 DFLVYINCKTMNKKODDLTYQTDFLATTSNMGFSGDKNELLIG-----AESFVSNKLY 640			
DT	01-MAR-2004 (TREMBLrel. 15, Last sequence update)		Db 552 ---MPLQKTMIEGENLTSRTPTRYTDSNIPSPRANPDDIGISEQPLTGAGS-ISSGRLY 605			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)		QY 641 YIDKIEFI 648			
DB	Toxin Ctry1Ca6.		Db 606 YIDKIEFI 613			
GN	Name=Ctry1Ca6;		RESULT 46			
OC	Bacillus thuringiensis.		Q6PYW7			
OC	Bacterium; Firmicutes; Bacillales; Bacillaceae; Bacillus.		ID Q6PYW7 PRELIMINARY;			
OX	NCBI TaxID:1428;		AC Q6PYW7 PRELIMINARY;			
RN	SEQUENCE FROM N.A.		DT 05-JUL-2004 (TREMBLrel. 27, Created)			
RP	STRAIN=2-F;		DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
RA	Yu J., Pang Y., Li J.;		DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
RL	Submitted (DB=1999) to the EMBL/GenBank/DBJ databases.		EMBL; ARF37224.1; -			

DE	CryIA type crystal protein (Fragment).	01-JAN-1988 (Rel. 06, Last sequence update)
OS	<i>Bacillus thuringiensis</i> (subsp. <i>kenyae</i>).	05-JUL-2004 (Rel. 44, Last annotation update)
OC	Bacteria; Firmicutes; <i>Bacillales</i> ; <i>Bacillaceae</i> ; <i>Bacillus</i> .	DE Pesticidal crystal protein CryIAb (Insecticidal delta-endotoxin).
NCBI_TaxID	33930;	DE CryIA (b) (Crystalline entomocidal protoxin) (130 kDa crystal protein).
[1]	SEQUENCE FROM N.A.	GN Name=CryIAb; Synonyms=bt2, cry-1-2, cryIA(b), cryIA(bt), cryICl;
RC	STRAIN=K3;	OS <i>Bacillus thuringiensis</i> (subsp. <i>kurstaki</i>)
RA	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;	OS <i>Bacillus thuringiensis</i> (subsp. <i>berliner</i>)
RA	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	OS <i>Bacillus thuringiensis</i> (subsp. <i>aizawai</i>).
DR	EMBL: AY570735; AAS93798; 1.;	OG Plasmid.
DR	GO: 0005102; F: receptor binding; IEA.	OG Bacterium; Firmicutes; <i>Bacillales</i> ; <i>Bacillaceae</i> ; <i>Bacillus</i> .
DR	GO: 0005952; P: defense response; IEA.	OC
DR	GO: 0009405; P: pathogenesis; IEA.	OX
DR	InterPro: IPR001178; Endotoxin.	RN [1] — TaxID=29339, 1434, 1433;
DR	InterPro: IPR005638; endotoxin C.	RP SEQDENCE FROM N.A.
DR	InterPro: IPR005639; endotoxin N.	RC SPECIES=B.t. <i>kurstaki</i> ; STRAIN=HD-1;
DR	InterPro: IPR008979; Gal bind Like.	MDLINE=87163505; PubMed=3557124; DOI=10.1016/0378-1119(86)90357-4;
DR	PFam; PF00344; Endotoxin_C; 1.	RX Geiser M., Schweiter S., Grimm C.; Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from <i>Bacillus thuringiensis</i> var. <i>kurstaki</i> HD-1 DNA. ".
DR	PFam; PF00555; Endotoxin_M; 1.	RA Hefford M.A., Brousseau R., Prefontaine G., Hanna Z., Condie J.A., Lau F.C.K.; "The hypervariable region in the genes coding for entomopathogenic crystal proteins of <i>Bacillus thuringiensis</i> : nucleotide sequence of the kurthi gene of subsp. <i>kurstaki</i> HD1.";
DR	PFam; PF003945; Endotoxin_N; 1.	RT Gene 48:109-118 (1986).
FT	NON_TER 793 793 AA; 89492 MW; 04F0DE79788E53DB CRC64;	RL RN [2]
FT	SEQUENCE 793 AA;	RP SEQUENCE FROM N.A.
FT	Score 909; DB 2; Length 793;	RC SPECIES=B.t. <i>kurstaki</i> ; STRAIN=HD-1;
Best Local Similarity	34.8%; Pred. No. 7.9e-5;	RA Kondo S., Tamura N., Kunitate A., Hattori M., Akashi A., Ohmori I.;
Matches	208; Conservative 114; Mismatches 210; Indels 66; Gaps 19;	RT "Cloning and nucleotide sequencing of two insecticidal delta-endotoxin genes from <i>Bacillus thuringiensis</i> var. <i>kurstaki</i> HD-1 DNA.";
QY	82 VPFAGALTSFYOSFLNTIW---PSDADPKAFMAQVEVILDKKIEBYAKSKALALQGL 137	RL Agric. Biol. Chem. 51:455-463 (1987).
QY	44 VPGAG---FVGLGLDINGIGFGSQ---WDAFLVQIEQLQINQRIEEFARNOAISRLEGI 96	RN [3]
QY	138 QNNFEDVYNALNSWKRTPLSLRSKRSQDRILFELFQASQESHRNMSFAYSFKFEVFLFLP 197	RP SEQUENCE FROM N.A.
Db	97 SNUQIYIAESFRAEADPTN-PALRVMHQ-IQ-FNDMNSALTTAILEFLAVQNYQVPLLSV 153	RC SPECIES=B.t. <i>kurstaki</i> ; STRAIN=HD-1;
QY	198 YAQAAANTHLLJKDAQVFGEEGNGSSDVAEFPYHQLKLTTQOYTDHCVNNTVNGLNLRG 257	MDLINE=86223796; PubMed=3011746;
Db	154 YQQAANTHLSVLRDVSVFGQRNGFDATTINSYRNLDLTRLIGNYTDIAVRWNTGLERWG 213	RA Thorne L., Gardiner F., Thompson T., Decker D., Zounes M., Wild M., Waller A.M., Pollock T.J.,
QY	258 STYDAWKPRNFRERMTLTVLDLIVPLPFYDILRYSKGKVTELTDLFTDPFLSNTLQ 317	RT "Structural similarity between the lepidoptera- and diptera-specific insecticidal endotoxin genes of <i>Bacillus thuringiensis</i> subsp. 'kurstaki' and 'israelensis'."
Db	214 PSDRWIYRNQFLERLTIVLDLIVPLFNPYDSRTYPIRTVSQLTREIYTPV---LED 268	RT J. Bacteriol. 166:801-811 (1986).
QY	318 YGPTF---LSTENSIRKPHLFPYLOGTEFTRPLQPSYFGKDSFNTWSGNVYETRPSIGS 373	RL RN [5]
Db	269 FNGSFRGSAQGIEQSIRSPLHMDILNSITTYDAHRYY----YNSGHQIMASPVGFS 322	RP SEQUENCE FROM N.A.
QY	374 SKTITSPFYGDK-STEPVQKLSFD-GKRYVRTANTDVAWPNKGKYLGVTKVDFSYQDD 431	RC SPECIES=B.t. <i>kurstaki</i> ; STRAIN=S93;
Db	323 379 TEPAYGTSNPLPSAVY---RKSCTV---DSLDEPPQNNTVPROGSRFLSHVSMFRSG 432	RA Silva-Wernick J.O., De-Souza M.T., Dias J.M.C.S., Ribeiro B.M.;
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RT "Characterization of <i>Bacillus thuringiensis</i> subsp. <i>kurstaki</i> strain S93 effective against the Fall armyworm, <i>Spodoptera frugiperda</i> and cloning of a cryAB gene."
Db	379 TEPAYGTSNPLPSAVY---RKSCTV---DSLDEPPQNNTVPROGSRFLSHVSMFRSG 432	RT Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RP SEQDENCE FROM N.A.
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RC SPECIES=B.t. <i>berliner</i> ; STRAIN=1715;
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQQLSVLDG 378	MDLINE=8630002; PubMed=3743328;
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RA Wabikko H., Raymond K.C., Bulla L.A. Jr.;
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQQLSVLDG 378	RT "Bacillus thuringiensis" entomocidal protoxin gene sequence and gene product analysis."
QY	541 LFLKRESSNNIAKEPKVTLNSAIIQLQYRTRIATSTNNRLFTYQ-----NSNNDFLYIY 594	RT DNA 5:305-314 (1986).
Db	493 541 L-RRTSPGQDISTLAVNI-TAPLSQRYTRVIRYAVSTTNLQFHTPSIDGRPINQGN-----F 544	RA Vaeck M.;
QY	595 545 NKTMNKDDDTYQFEDLTATNSNMGKDNELIGAEVNEKTYDKEFIPVOL 652	RT "Structural and functional analysis of a cloned delta endotoxin of <i>Bacillus thuringiensis</i> berliner 175."
Db	545 SATMSSGSNLQSGSFRTAGFTPPNFNSGSSVFTLSAHHFNSGNEVIRDEFVPAEV 602	RT Eur. J. Biochem. 161:273-280 (1986).
RE	RESULT 47	RL RN [8]
C1	C1_BACTK	RP SEQUENCE FROM N.A.
ID	C1AB_BACTK	RC
AC	P06578; P06577; P09663; P09666; P21257;	RX
DB	545 SATMSSGSNLQSGSFRTAGFTPPNFNSGSSVFTLSAHHFNSGNEVIRDEFVPAEV 602	RA
DT	01-JAN-1988 (Rel. 06, Last sequence update)	RA
DT	05-JUL-2004 (Rel. 44, Last annotation update)	RA
DE	Pesticidal crystal protein CryIAb (Insecticidal delta-endotoxin).	RA
DE	CryIA (b) (Crystalline entomocidal protoxin) (130 kDa crystal protein).	RA
GN	Name=CryIAb; Synonyms=bt2, cry-1-2, cryIA(b), cryICl;	RA
OS	<i>Bacillus thuringiensis</i> (subsp. <i>berliner</i>)	RA
OS	<i>Bacillus thuringiensis</i> (subsp. <i>aizawai</i>).	RA
OG	Plasmid.	RA
OG	Bacterium; Firmicutes; <i>Bacillales</i> ; <i>Bacillaceae</i> ; <i>Bacillus</i> .	RA
OC		RA
NCBI_TaxID		RA
[1]	SEQUENCE FROM N.A.	RA
RC	STRAIN=K3;	RA
RA	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;	RA
RA	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	RA
DR	EMBL: AY570735; AAS93798; 1.;	RA
DR	GO: 0005102; F: receptor binding; IEA.	RA
DR	GO: 0005952; P: defense response; IEA.	RA
DR	GO: 0009405; P: pathogenesis; IEA.	RA
DR	InterPro: IPR001178; Endotoxin.	RA
DR	InterPro: IPR005638; endotoxin C.	RA
DR	InterPro: IPR005639; endotoxin N.	RA
DR	InterPro: IPR008979; Gal bind Like.	RA
DR	PFam; PF00344; Endotoxin_C; 1.	RA
DR	PFam; PF00555; Endotoxin_M; 1.	RA
DR	PFam; PF003945; Endotoxin_N; 1.	RA
FT	NON_TER 793 793 AA; 89492 MW; 04F0DE79788E53DB CRC64;	RA
FT	SEQUENCE 793 AA;	RA
FT	Score 909; DB 2; Length 793;	RA
Best Local Similarity	34.8%; Pred. No. 7.9e-5;	RA
Matches	208; Conservative 114; Mismatches 210; Indels 66; Gaps 19;	RA
QY	82 VPFAGALTSFYOSFLNTIW---PSDADPKAFMAQVEVILDKKIEBYAKSKALALQGL 137	RA
QY	44 VPGAG---FVGLGLDINGIGFGSQ---WDAFLVQIEQLQINQRIEEFARNOAISRLEGI 96	RA
QY	138 QNNFEDVYNALNSWKRTPLSLRSKRSQDRILFELFQASQESHRNMSFAYSFKFEVFLFLP 197	RA
Db	97 SNUQIYIAESFRAEADPTN-PALRVMHQ-IQ-FNDMNSALTTAILEFLAVQNYQVPLLSV 153	RA
QY	198 YAQAAANTHLLJKDAQVFGEEGNGSSDVAEFPYHQLKLTTQOYTDHCVNNTVNGLNLRG 257	RA
Db	154 YQQAANTHLSVLRDVSVFGQRNGFDATTINSYRNLDLTRLIGNYTDIAVRWNTGLERWG 213	RA
QY	258 STYDAWKPRNFRERMTLTVLDLIVPLPFYDILRYSKGKVTELTDLFTDPFLSNTLQ 317	RA
Db	214 PSDRWIYRNQFLERLTIVLDLIVPLFNPYDSRTYPIRTVSQLTREIYTPV---LED 268	RA
QY	318 YGPTF---LSTENSIRKPHLFPYLOGTEFTRPLQPSYFGKDSFNTWSGNVYETRPSIGS 373	RA
Db	269 FNGSFRGSAQGIEQSIRSPLHMDILNSITTYDAHRYY----YNSGHQIMASPVGFS 322	RA
QY	374 SKTITSPFYGDK-STEPVQKLSFD-GKRYVRTANTDVAWPNKGKYLGVTKVDFSYQDD 431	RA
Db	323 379 TEPAYGTSNPLPSAVY---RKSCTV---DSLDEPPQNNTVPROGSRFLSHVSMFRSG 432	RA
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RA
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQQLSVLDG 378	RA
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RA
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQQLSVLDG 378	RA
QY	541 LFLKRESSNNIAKEPKVTLNSAIIQLQYRTRIATSTNNRLFTYQ-----NSNNDFLYIY 594	RA
Db	493 541 L-RRTSPGQDISTLAVNI-TAPLSQRYTRVIRYAVSTTNLQFHTPSIDGRPINQGN-----F 544	RA
QY	595 NKTMNKDDDTYQFEDLTATNSNMGKDNELIGAEVNEKTYDKEFIPVOL 652	RA
Db	545 SATMSSGSNLQSGSFRTAGFTPPNFNSGSSVFTLSAHHFNSGNEVIRDEFVPAEV 602	RA
RE	RESULT 47	RA
C1	C1_BACTK	RC
ID	C1AB_BACTK	RX
AC	P06578; P06577; P09663; P09666; P21257;	RA
DB	545 SATMSSGSNLQSGSFRTAGFTPPNFNSGSSVFTLSAHHFNSGNEVIRDEFVPAEV 602	RA
DT	01-JAN-1988 (Rel. 06, Last sequence update)	RA
DT	05-JUL-2004 (Rel. 44, Last annotation update)	RA
DE	Pesticidal crystal protein CryIAb (Insecticidal delta-endotoxin).	RA
DE	CryIA (b) (Crystalline entomocidal protoxin) (130 kDa crystal protein).	RA
GN	Name=CryIAb; Synonyms=bt2, cry-1-2, cryIA(b), cryICl;	RA
OS	<i>Bacillus thuringiensis</i> (subsp. <i>berliner</i>)	RA
OS	<i>Bacillus thuringiensis</i> (subsp. <i>aizawai</i>).	RA
OG	Plasmid.	RA
OG	Bacterium; Firmicutes; <i>Bacillales</i> ; <i>Bacillaceae</i> ; <i>Bacillus</i> .	RA
OC		RA
NCBI_TaxID		RA
[1]	SEQUENCE FROM N.A.	RA
RC	STRAIN=K3;	RA
RA	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;	RA
RA	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	RA
DR	EMBL: AY570735; AAS93798; 1.;	RA
DR	GO: 0005102; F: receptor binding; IEA.	RA
DR	GO: 0005952; P: defense response; IEA.	RA
DR	GO: 0009405; P: pathogenesis; IEA.	RA
DR	InterPro: IPR001178; Endotoxin.	RA
DR	InterPro: IPR005638; endotoxin C.	RA
DR	InterPro: IPR005639; endotoxin N.	RA
DR	InterPro: IPR008979; Gal bind Like.	RA
DR	PFam; PF00344; Endotoxin_C; 1.	RA
DR	PFam; PF00555; Endotoxin_M; 1.	RA
DR	PFam; PF003945; Endotoxin_N; 1.	RA
FT	NON_TER 793 793 AA; 89492 MW; 04F0DE79788E53DB CRC64;	RA
FT	SEQUENCE 793 AA;	RA
FT	Score 909; DB 2; Length 793;	RA
Best Local Similarity	34.8%; Pred. No. 7.9e-5;	RA
Matches	208; Conservative 114; Mismatches 210; Indels 66; Gaps 19;	RA
QY	82 VPFAGALTSFYOSFLNTIW---PSDADPKAFMAQVEVILDKKIEBYAKSKALALQGL 137	RA
QY	44 VPGAG---FVGLGLDINGIGFGSQ---WDAFLVQIEQLQINQRIEEFARNOAISRLEGI 96	RA
QY	138 QNNFEDVYNALNSWKRTPLSLRSKRSQDRILFELFQASQESHRNMSFAYSFKFEVFLFLP 197	RA
Db	97 SNUQIYIAESFRAEADPTN-PALRVMHQ-IQ-FNDMNSALTTAILEFLAVQNYQVPLLSV 153	RA
QY	198 YAQAAANTHLLJKDAQVFGEEGNGSSDVAEFPYHQLKLTTQOYTDHCVNNTVNGLNLRG 257	RA
Db	154 YQQAANTHLSVLRDVSVFGQRNGFDATTINSYRNLDLTRLIGNYTDIAVRWNTGLERWG 213	RA
QY	258 STYDAWKPRNFRERMTLTVLDLIVPLPFYDILRYSKGKVTELTDLFTDPFLSNTLQ 317	RA
Db	214 PSDRWIYRNQFLERLTIVLDLIVPLFNPYDSRTYPIRTVSQLTREIYTPV---LED 268	RA
QY	318 YGPTF---LSTENSIRKPHLFPYLOGTEFTRPLQPSYFGKDSFNTWSGNVYETRPSIGS 373	RA
Db	269 FNGSFRGSAQGIEQSIRSPLHMDILNSITTYDAHRYY----YNSGHQIMASPVGFS 322	RA
QY	374 SKTITSPFYGDK-STEPVQKLSFD-GKRYVRTANTDVAWPNKGKYLGVTKVDFSYQDD 431	RA
Db	323 379 TEPAYGTSNPLPSAVY---RKSCTV---DSLDEPPQNNTVPROGSRFLSHVSMFRSG 432	RA
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RA
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQQLSVLDG 378	RA
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RA
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQQLSVLDG 378	RA
QY	541 LFLKRESSNNIAKEPKVTLNSAIIQLQYRTRIATSTNNRLFTYQ-----NSNNDFLYIY 594	RA
Db	493 541 L-RRTSPGQDISTLAVNI-TAPLSQRYTRVIRYAVSTTNLQFHTPSIDGRPINQGN-----F 544	RA
QY	595 NKTMNKDDDTYQFEDLTATNSNMGKDNELIGAEVNEKTYDKEFIPVOL 652	RA
Db	545 SATMSSGSNLQSGSFRTAGFTPPNFNSGSSVFTLSAHHFNSGNEVIRDEFVPAEV 602	RA
RE	RESULT 47	RA
C1	C1_BACTK	RC
ID	C1AB_BACTK	RX
AC	P06578; P06577; P09663; P09666; P21257;	RA
DB	545 SATMSSGSNLQSGSFRTAGFTPPNFNSGSSVFTLSAHHFNSGNEVIRDEFVPAEV 602	RA
DT	01-JAN-1988 (Rel. 06, Last sequence update)	RA
DT	05-JUL-2004 (Rel. 44, Last annotation update)	RA
DE	Pesticidal crystal protein CryIAb (Insecticidal delta-endotoxin).	RA
DE	CryIA (b) (Crystalline entomocidal protoxin) (130 kDa crystal protein).	RA
GN	Name=CryIAb; Synonyms=bt2, cry-1-2, cryIA(b), cryICl;	RA
OS	<i>Bacillus thuringiensis</i> (subsp. <i>berliner</i>)	RA
OS	<i>Bacillus thuringiensis</i> (subsp. <i>aizawai</i>).	RA
OG	Plasmid.	RA
OG	Bacterium; Firmicutes; <i>Bacillales</i> ; <i>Bacillaceae</i> ; <i>Bacillus</i> .	RA
OC		RA
NCBI_TaxID		RA
[1]	SEQUENCE FROM N.A.	RA
RC	STRAIN=K3;	RA
RA	Li M.S., Choi J.Y., Roh J.Y., Shim H.J., Boo K.S., Je Y.H.;	RA
RA	Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.	RA
DR	EMBL: AY570735; AAS93798; 1.;	RA
DR	GO: 0005102; F: receptor binding; IEA.	RA
DR	GO: 0005952; P: defense response; IEA.	RA
DR	GO: 0009405; P: pathogenesis; IEA.	RA
DR	InterPro: IPR001178; Endotoxin.	RA
DR	InterPro: IPR005638; endotoxin C.	RA
DR	InterPro: IPR005639; endotoxin N.	RA
DR	InterPro: IPR008979; Gal bind Like.	RA
DR	PFam; PF00344; Endotoxin_C; 1.	RA
DR	PFam; PF00555; Endotoxin_M; 1.	RA
DR	PFam; PF003945; Endotoxin_N; 1.	RA
FT	NON_TER 793 793 AA; 89492 MW; 04F0DE79788E53DB CRC64;	RA
FT	SEQUENCE 793 AA;	RA
FT	Score 909; DB 2; Length 793;	RA
Best Local Similarity	34.8%; Pred. No. 7.9e-5;	RA
Matches	208; Conservative 114; Mismatches 210; Indels 66; Gaps 19;	RA
QY	82 VPFAGALTSFYOSFLNTIW---PSDADPKAFMAQVEVILDKKIEBYAKSKALALQGL 137	RA
QY	44 VPGAG---FVGLGLDINGIGFGSQ---WDAFLVQIEQLQINQRIEEFARNOAISRLEGI 96	RA
QY	138 QNNFEDVYNALNSWKRTPLSLRSKRSQDRILFELFQASQESHRNMSFAYSFKFEVFLFLP 197	RA
Db	97 SNUQIYIAESFRAEADPTN-PALRVMHQ-IQ-FNDMNSALTTAILEFLAVQNYQVPLLSV 153	RA
QY	198 YAQAAANTHLLJKDAQVFGEEGNGSSDVAEFPYHQLKLTTQOYTDHCVNNTVNGLNLRG 257	RA
Db	154 YQQAANTHLSVLRDVSVFGQRNGFDATTINSYRNLDLTRLIGNYTDIAVRWNTGLERWG 213	RA
QY	258 STYDAWKPRNFRERMTLTVLDLIVPLPFYDILRYSKGKVTELTDLFTDPFLSNTLQ 317	RA
Db	214 PSDRWIYRNQFLERLTIVLDLIVPLFNPYDSRTYPIRTVSQLTREIYTPV---LED 268	RA
QY	318 YGPTF---LSTENSIRKPHLFPYLOGTEFTRPLQPSYFGKDSFNTWSGNVYETRPSIGS 373	RA
Db	269 FNGSFRGSAQGIEQSIRSPLHMDILNSITTYDAHRYY----YNSGHQIMASPVGFS 322	RA
QY	374 SKTITSPFYGDK-STEPVQKLSFD-GKRYVRTANTDVAWPNKGKYLGVTKVDFSYQDD 431	RA
Db	323 379 TEPAYGTSNPLPSAVY---RKSCTV---DSLDEPPQNNTVPROGSRFLSHVSMFRSG 432	RA
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RA
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQQLSVLDG 378	RA
QY	486 DRGTI---YDSKRNGNHVSAQSDISOLPPTTDEPKAYQHQNAYAECFLMQ 485	RA
Db	433 323 GPBFTPLXGTMGNAAPQORIVAAQLGQEVYRTSST---FVRSFPNIGNNQ	

RC	SPECIES=B.t.aizawai; STRAIN=HD-133;	PT	CONFFLICT	410	410	L -> P (in Ref. 4).
RA	Chak K.-F., Jen J.-C.;	LSH	-> CLAY (in Ref. 4).			
RT	"Complete nucleotide sequence and identification of a putative promoter region for the expression in Escherichia coli of the cryIA(b) gene from <i>Bacillus thuringiensis</i> var. aizawai HD133.";	R	-> Y (in Ref. 4).			
RT	Proc. Natl. Sci. Counc. Repub. China, B, Life Sci. 17:7-14 (1993).	I	-> V (in Ref. 4).			
RN	[19]	A	-> P (in Ref. 10).			
SEQUENCE FROM N.A.	SEQUENCE FROM N.A.	MFSWIHR	-> NDSSWTRIC (in Ref. 4).			
RC	SPECIES=B.t.aizawai; STRAIN=IC1;	E	-> N (in Ref. 3).			
RC	SEQUENCE FROM N.A.	NNI	-> GDV (in Ref. 4).			
RP	SEQUENCE FROM N.A.	SPNLGSGT	-> LOSWLN (in Ref. 4).			
RX	Medline=87248103; PubMed=3297927; DOI=10.1016/0378-1119(87)90098-9;	PT	CONFFLICT	430	432	P -> L (in Ref. 4).
RA	Oeda K., Ohnishi K., Shimizu M., Nakamoto H., Nakayama I.,	PT	CONFFLICT	437	437	R -> Y (in Ref. 4).
RA	Ohkawa H.;	PT	CONFFLICT	447	447	I -> V (in Ref. 4).
RT	"Nucleotide sequence of the insecticidal protein gene of <i>Bacillus thuringiensis</i> strain aizawai 1p7 and its high-level expression in <i>Escherichia coli</i> .";	PT	CONFFLICT	450	450	A -> P (in Ref. 10).
RT	Gene 53:113-119 (1987).	PT	CONFFLICT	452	458	MFSWIHR
RL	[10]	PT	CONFFLICT	461	461	-> N (in Ref. 3).
RN	"Nucleotide sequence of a <i>Bacillus thuringiensis</i> aizawai 1C1 entomocidal crystal protein gene.";	PT	CONFFLICT	463	465	NNI -> GDV (in Ref. 4).
RP	SEQUENCE FROM N.A.	PT	CONFFLICT	479	486	SPNLGSGT -> LOSWLN (in Ref. 4).
RX	Medline=89083518; PubMed=3205732;	PT	CONFFLICT	492	492	P -> L (in Ref. 4).
RA	Halder M.Z., Eillat D.J.;	PT	CONFFLICT	501	505	RTRSP -> EELT (in Ref. 4).
RA	"Nucleotide sequence of a <i>Bacillus thuringiensis</i> aizawai 1C1 entomocidal crystal protein gene.";	PT	CONFFLICT	537	537	F -> L (in Ref. 10).
RT	Nucleic Acids Res 16:10927-10927-1998.	PT	CONFFLICT	542	542	D -> H (in Ref. 3).
CC	-1- FUNCTION: Promotes colicidiodsmotic lysis by binding to the midgut epithelial cells of many lepidopteran larvae.	PT	CONFFLICT	545	545	D -> I (in Ref. 10).
CC	-1- DEVELOPMENTAL STAGE: The crystal protein is produced during sporulation and is accumulated both as an inclusion and as part of the spore coat.	PT	CONFFLICT	568	568	T -> I (in Ref. 10).
CC	-1- BIOTECHNOLOGY: Introduced by genetic manipulation and expressed in insect -resistant maize by Monsanto, Northrup King and Ciba Geigy.	PT	CONFFLICT	569	569	TV -> HL (in Ref. 3).
CC	-1- MISCELLANEOUS: Toxic segment of the protein is located in the N-terminus.	PT	CONFFLICT	665	665	P -> R (in Ref. 7 and 10).
CC	-1- SIMILARITY: Belongs to the delta endotoxin family.	PT	CONFFLICT	675	676	K -> S (in Ref. 3).
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions. As long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	PT	CONFFLICT	703	703	KR -> NG (in Ref. 3).
CC	DR	PT	CONFFLICT	712	712	S -> N (in Ref. 4).
CC	DR	PT	CONFFLICT	731	731	P -> L (in Ref. 4).
CC	DR	PT	CONFFLICT	785	785	P -> R (in Ref. 7 and 10).
CC	DR	PT	CONFFLICT	836	836	P -> R (in Ref. 3).
CC	DR	PT	CONFFLICT	978	978	N -> I (in Ref. 3).
CC	DR	PT	CONFFLICT	1016	1016	H -> Q (in Ref. 9).
CC	DR	PT	CONFFLICT	1036	1036	E -> T (in Ref. 3).
CC	DR	PT	CONFFLICT	1060	1060	C -> F (in Ref. 9).
CC	DR	SEQUENCE	1155 AA;	130623 MW;	43461A64C7AC7CAF	CRC64;
CC	DR	Query Match	26.4%	Score 899.5;	DB 1;	Length 1155;
CC	DR	Best Local Similarity	33.3%	Pred. No. 5.6e-50;		
CC	DR	Matches 220;	Conservative	118;	Missmatches 231;	Indels 91; Gaps 24;
CC	DR	Qy	31	DNPNSTLLELNKEFELMTEEDSSTEVDNSTVYKDAVGTGIVSVG-----QILGVGVPF	84	
CC	DR	Db	3	NNPNIN-ECIP-----NCLSNPEVEVGLGERIE-----TGYTPIDISLSLTQFNLSEFVPG	53	
CC	DR	Qy	85	AGALTISFYQSFLNTIW----PSDADPKAFAQVVEVLDDKKEBEYAKSKALAEGLGLNN	140	
CC	DR	Db	54	AG----FVGLVDIIMGFQFQSQ----WDAFLVQIEQLINQRIEEFARNOAISRLEGLSNL	106	
CC	DR	Qy	141	FEDYVNALNSWKRKTPSLRSKRSQDRLEFLGQAEHSFRNSMSFAVSKFEVLFPLTYAQ	200	
CC	DR	Db	107	YQIYAESTREWEADPTN-PALREEMRQ--FNDMSNALSATTAIPFLAVQNYQVLLSVRYQ	163	
CC	DR	Qy	201	AANTHLLJLKDQVFGEWGKSEEDVAFYHQRLKLTQOYTHCWNVYNNGLNGLRGSTY	260	
CC	DR	Db	164	AANLHSVLRDVSFVGWRGDAATINSRNNDLTLRIGNTYDHAIRGEY-----YWSGHOIMASPVFGSGPE	223	
CC	DR	Qy	261	DAWKFNFRFRENTLTIVLULFPYDILRYSKGVKTELTDITDPISLNTLQEYGP	320	
CC	DR	Db	224	RDWIRYQFRRELTIVLULIVSLFNPYDSRTRPITYSVQLTREIYTFV-----LENFDG	278	
CC	DR	Qy	321	TF----LSIENSRSRKHFLFDYLGQIEPHTRLOGYFRGDSFNYWSGNVETRPSIGSSRT	376	
CC	DR	Db	279	SFGFSAGGIEGSTRSPHLMIDLNSITIYTDAHGEY-----YWSGHOIMASPVFGSGPE	332	
CC	DR	Qy	377	ITSPPYGDK-STEPVQKLSEFD-GQKYYRTIANTDVAAWPNKGKVY-----LGITTKVDFRQY	429	
CC	DR	Db	333	FTPLPLYGMGNAAQDQRIVAQGQGVRTLSS-----LYRPRPNIGNNQQLSVL	383	
CC	DR	Qy	430	DDQKNETSTQT-----YDSKRNNNGHVAQDSIDQLPPTTDEPLEKAYSHQLNAYAECFL	483	
CC	DR	Db	384	DGEFAYGTSSNLPSSAVY--RKGSTV--DSUDEIPQNNNNVPRQGFSHRLSHVSMFR	437	
CC	DR	Qy	484	MDRRGTI-----PFFTWTHRSVDFPFTDAEKITDLPVRYALSSASILEGPGFPTGG	538	
CC	DR	Db	438	SQFSNNSVSIIRAPMFSWIRSAEENNIPSSQQTQPLTKSTNLGSCTSVKGPGFPTGG	497	
CC	DR	Qy	539	NLFLEKSSNSAIAKFTYLTNSALLOQYVRVRYAATNLRLFVQ-----NSNNNDFLAVI	592	
CC	DR	Db	498	DIL-RTRSPGQ1STLRVNI-TAPLSQRYVRVRYAATNLQFHTSDGRPINQGN-----LKPGQQPTEKABP	550	

Qy	593 YINKTMKDDLTYYQTFPLATTNSMGFSGDKNELIGAESFSNEKIXYIDKIEFIPVQL 652	Qy	430 DDQKNEFTSTQT-----YDSKRNNGGHVSQAQPSIDQFLPPTDEPLEKAYSHOLNYAECFL 483
Db	551 -FSATMSSGSNLQSGSFRTVGFPTPENGSVFTISATVFNNSGNVEIVIDRIEFVPAEV 609	Db	384 DGTEFNGTSNLPSAVY--RKSFGV--DSLDEPPQNINVPFGQFSRSLSHSISMFR 437
RESULT 48		RESLT 48	
Q7BE98	PRELIMINARY;	Q7BE98	PRELIMINARY;
ID	PRT; 1155 AA.	ID	PRT; 1155 AA.
AC	Li C., Zhang J., Ji G., Huang D.;	AC	Q9F296; PRELIMINARY;
DT	05-JUL-2004 (TREMBLrel. 27, Created)	DT	Q9F296; PRELIMINARY;
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DE	Crystal endotoxin Cry1Ab (Insecticidal protein P).	DE	Delta endotoxin.
GN	Name=cry1Ab	GN	YINKTMKDDLTYYQTFPLATTNSMGFSGDKNELIGAESFSNEKIXYIDKIEFIPVQL 652
OS	Bacillus thuringiensis.	OS	593 YINKTMKDDLTYYQTFPLATTNSMGFSGDKNELIGAESFSNEKIXYIDKIEFIPVQL 652
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	OC	551 -FSATMSSGSNLQSGSFRTVGFPTPENGSVFTISATVFNNSGNVEIVIDRIEFVPAEV 609
OX	NCBI_TaxID=1428;	OX	
RN	[1]	RN	RESULT 49
RP	SEQUENCE FROM N.A.	RP	Q9F296
RC	STRAIN=B-Hm-16;	RC	ID
RA	Li C., Zhang J., Ji G., Huang D.;	RA	Q9F296;
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.	RL	AC
[2]	SEQUENCE FROM N.A.	[2]	DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
RN		RN	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
RP		RP	
RC	STRAIN=BTC005;	RC	
RA	Tan J., Zhang J., Wang K., Huang D.;	RA	
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.	RL	
EMBL; AF358861; AA013302.1;	EMBL; AF358861; AA013302.1;	EMBL; U94191; AAC16877.1;	SEQUENCE FROM N.A.
EMBL; AF254540; AA076494.1;	EMBL; AF254540; AA076494.1;	EMBL; U94191; AAC16877.1;	Meza-Basbo L.A., Theodoulou C.; Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR	GO: GO:0005102; F: receptor binding; IEA.	DR	DR
DR	GO: GO:0006952; P: defense response; IEA.	DR	DR
DR	GO: GO:0005045; P: pathogenesis; IEA.	DR	DR
DR	InterPro: IPR001178; Endotoxin.	DR	DR
DR	InterPro: IPR005638; endotoxin.	DR	DR
DR	InterPro: IPR005639; endotoxin.	DR	DR
DR	InterPro: IPR008979; Gal bind like.	DR	DR
DR	Pfam; PF03944; Endotoxin_C_1.	DR	DR
DR	Pfam; PF03945; Endotoxin_M_1.	DR	DR
DR	Pfam; PF03945; Endotoxin_N_1.	DR	DR
SQ	SEQUENCE 1155 AA; 130623 MW; 43461A64C7ACTCAF CRC64;	SQ	SEQUENCE 1155 AA; 130557 MW; 5D969E52F527749D CRC44;
Qy	31 DNPNSTLEELNYKEFLRMTEDSSTEVLDSNTVKDAVTGTSVGV----QILGVGVGP 84	Qy	31 DNPNSTLEELNYKEFLRMTEDSSTEVLDSNTVKDAVTGTSVGV----QILGVGVGP 84
Db	3 NNPNTN-ECIY---NCLSNPBEVLLGGERIE---TGTPIDISLSTQFLLSEFVPG 53	Db	3 NNPNTN-ECIY---NCLSNPBEVLLGGERIE---TGTPIDISLSTQFLLSEFVPG 53
Qy	85 AGALTSPYQSFINTIW---PDADEPKWFAQVEVLIDKLEEYAKSKALAEQQLQNN 140	Qy	85 AGALTSPYQSFINTIW---PDADEPKWFAQVEVLIDKLEEYAKSKALAEQQLQNN 140
Db	54 AG---FVGLVLDIINGIFGP SQ--.WDAFLVQIEQLINQRIEFARNQASRLECLSNL 106	Db	54 AG---FVGLVLDIINGIFGP SQ--.WDAFLVQIEQLINQRIEFARNQASRLECLSNL 106
Qy	141 FEDYVNALNSWKTKPLSLRSRSQDRITRELFSQAESHFRNMSPFAVSKFVFLPTYAQ 200	Qy	141 FEDYVNALNSWKTKPLSLRSRSQDRITRELFSQAESHFRNMSPFAVSKFVFLPTYAQ 200
Db	1.07 YQIYAESFREADEPTN-PALEBEMRIO- FMDMNSALTAITPLFAVQNCVPLSVYQ 163	Db	1.07 YQIYAESFREADEPTN-PALEBEMRIO- FMDMNSALTAITPLFAVQNCVPLSVYQ 163
Qy	201 AANTHLLKDAQVFGEGWYSSDEAEEYHRQLKLTQQTQDHCWNYWYNGLNGRSTY 260	Qy	201 AANTHLLKDAQVFGEGWYSSDEAEEYHRQLKLTQQTQDHCWNYWYNGLNGRSTY 260
Db	164 AANLHSLSVLRDVSFGQRWGFDAATINSRNDRTRIIGNYTDHAWRYNTGLERWGPDS 223	Db	164 AANLHSLSVLRDVSFGQRWGFDAATINSRNDRTRIIGNYTDHAWRYNTGLERWGPDS 223
Qy	261 DAWKCNPARREMILTVLDLIVLWPLFPFDYRLYQGIEFHTLQGKVKTELDITDPIISLNTQOBYGP 320	Qy	261 DAWKCNPARREMILTVLDLIVLWPLFPFDYRLYQGIEFHTLQGKVKTELDITDPIISLNTQOBYGP 320
Db	224 RDWIRYNQFRELTLTVLDLIVLWPLFPFDYRLYQGIEFHTLQGKVKTELDITDPIISLNTQOBYGP 278	Db	224 RDWIRYNQFRELTLTVLDLIVLWPLFPFDYRLYQGIEFHTLQGKVKTELDITDPIISLNTQOBYGP 278
Qy	321 TF---LSIENSIRKPHLFYQGIEFHTLQGKVKTELDITDPIISLNTQOBYGP 376	Qy	321 TF---LSIENSIRKPHLFYQGIEFHTLQGKVKTELDITDPIISLNTQOBYGP 376
Db	279 SFRGSAQIGESIRSIRSPHMLDILNSITYTDHARGEY----YWSQHQIMASPVGFSGGP 332	Db	279 SFRGSAQIGESIRSIRSPHMLDILNSITYTDHARGEY----YWSQHQIMASPVGFSGGP 332
Qy	377 ITSPFGDK-STEPVOKLSDQKTYRTIANTDVAAPNGKRY----LGVTKVDFDSQY 429	Qy	377 ITSPFGDK-STEPVOKLSDQKTYRTIANTDVAAPNGKRY----LGVTKVDFDSQY 429
Db	333 FTFPLXTGMGNAAQORIVAAQLGQGQYRTLSST-----LYRRPENGINNOOLSVL 383	Db	333 FTFPLXTGMGNAAQORIVAAQLGQGQYRTLSST-----LYRRPENGINNOOLSVL 383

Db 279 SFRGSAQGLEGGSIRSPLHMDILNSITIYDAHREGYE-----YWSGHQIMASPVGFSGFB 332
 Qy 377 ITSPYGDK-K-STEVPQKLSSD-GQKVRYRINTDVAWWNGKVV-----LGVTKVDFSY 429
 Db 333 FTFFPLYGMCGNAAPQRIYAQLGGCVYRILST-----LYRPFNIGINNQQLSVL 383
 Qy 430 DDQKNETST-----YDSKRANGHVSQADSDTQDLPPTTDEPLEKAYSHOLNYAECFL 483
 Db 384 DGTEPAYGSSNLPASVY---RKSCTV---DSLDEIPRQNNNVPQROGSHRLSHVSMR 437
 Qy 484 MDQRRGTI-----PFPFTWTHRSVDFFNTIDAEEKITQDLPVTKAYALSSGSSIICPGFTGG 538
 Db 438 SGFNSNSVSVTIRAPMSWTHRSAEENNIIPLSSQITQIPLTKSTNLGSGTSVVKPGFTGG 497
 Qy 539 NLLFLKESNSNSIAKEPKVTNSAALIQLRYVRVIRYVASTTNLRLFVQ-----NSNNDFLV 592
 Db 498 DIL-RRTSGDQQISTLRVN1-TAPLSQRYVRVIRYVASTTNLQFHTSIDGRPINQCN-----550
 Qy 593 YINKTMNKDDDLTYQTDFLATTNSMGSGDKNEELIGAESFSYNEKLYIDKLEFIPVQL 652
 Db 551 -FSATMSSGSNLQSSSFRTVGFITPPFNFGSSYFTLSAHLVFNSGNEYVDRFVPAEV 609
 Db 552 YINKTMNKDDDLTYQTDFLATTNSMGSGDKNEELIGAESFSYNEKLYIDKLEFIPVQL 652
 Qy 551 -FSATMSSGSNLQSSSFRTVGFITPPFNFGSSYFTLSAHLVFNSGNEYVDRFVPAEV 609
 Db 552 YINKTMNKDDDLTYQTDFLATTNSMGSGDKNEELIGAESFSYNEKLYIDKLEFIPVQL 652
 Qy 551 -FSATMSSGSNLQSSSFRTVGFITPPFNFGSSYFTLSAHLVFNSGNEYVDRFVPAEV 609

RESULT 50

Q66UA7 ID Q66UA7 PRELIMINARY; PRT; 1156 AA.

AC Q66UA7; PRELIMINARY;

DT 05-JUL-2004 (TREMBurel, 27, Created)
 DT 05-JUL-2004 (TREMBurel, 27, Last sequence update)
 DT 05-JUL-2004 (TREMBurel, 27, Last annotation update)

DE Paraspoxal crystal protein.

OS Bacillus thuringiensis.

OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.

OX NCBI_TaxID=1428;

RN [1]

RP SEQUENCE FROM N.A.;

RA Huang Z., Guan C., Guan X.;

RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; A164616; ART46415.1;

DR GO:0005102; F receptor binding; IBA.

DR GO:0006932; P defense response; IBA.

DR GO:0009405; P pathogenesis; IBA.

DR InterPro: IPR0011178; Endotoxin.

DR InterPro: IPR005638; endotoxin_C.

DR InterPro: IPR005639; endotoxin_N.

DR InterPro: IPR008919; Gal_biotin_Like.

DR Pfam; PF03944; Endotoxin_C.

DR Pfam; PF00545; Endotoxin_M.

DR Pfam; PF03945; Endotoxin_N.

SQ SEQUENCE 1156 AA; 130533 MW; 1759B23E3DAA4A09 CRC64;

Query Match 26.4%; Score 898.5; DB 2; Length 1156;
 Best Local Similarity 33.3%; Pred. No. 6.5e-50;
 Matches 220; Conservative 118; Mismatches 231; Indels 91; Gaps 24;

Qy 31 DNPNTSLEFLNPKFLRMTEDSSTEVLDSNTVDAVGTCISVVG-----QILGVGVGP F 84
 Db 3 NNPNTN-ECIPIY----NCIISNPETEVLGBERIE----TCYTPIDISLSLTOFLSEFVG 53

Qy 85 AGALTTSFYQFLNITW----PSDADPWFKAQVEVLIDKKEBAYAKSKALABQGLQNN 140
 Db 54 AG---FVIGLVDIINGTGPSQ --WDNFLVQIEQLINQRIEPFARNQAIISLEGSLNL 106

Qy 141 FEDTNALNSWKCKTPLSLRSKRSQDRINFLPSQAESHRNSMSFAVSKFEVFLPFIYA Q 200
 Db 107 YQ1YAESFWEADPTN-FALERFEMRQ---FNDKNSALTAUPLFAYVQYQPLLSYYVQ 163

Qy 201 AANTHLLIKDAQVGEGEVGSSSEDAEYTHRQLKLTOQYTDHCWNWVNGLRLSSTY 260
 Db 164 AANLHLPLVLRDVSFGQRMGFDAATINSRSYNDLTRLIGNTYDIAVRVNTGLERVWGFDS 223
 Qy 261 DAWYKFNRRFRREMTLTVLPLIVLPPFYDRLYSLRGVKTFLDIFTDPIFSINTLQYGP 320

THIS PAGE BLANK (USPTO)